; PRIOR FILING DATE: 1993-10-14
; PRIOR APPLICATION NUMBER: 08/197,801
; PRIOR FILING DATE: 1994-02-17
; PRIOR APPLICATION NUMBER: 08/237,491
; PRIOR FILING DATE: 1994-04-28
; PRIOR APPLICATION NUMBER: 08/296,757
; PRIOR FILING DATE: 1994-08-26
; PRIOR APPLICATION NUMBER: 08/221,531
; PRIOR FILING DATE: 1994-02-02
; PRIOR APPLICATION NUMBER: 08/435,761
; PRIOR FILING DATE: 1995-05-05
; PRIOR APPLICATION NUMBER: 08/194,317
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; PRIOR FILING DATE: 1995-06-07
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; PRIOR FILING DATE: 1994-06-27
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; PRIOR FILING DATE: 1995-08-16
; PRIOR APPLICATION NUMBER: 08/274,621
; PRIOR FILING DATE: 1994-07-08
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; PRIOR FILING DATE: 1995-03-29
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; PRIOR FILING DATE: 1994-07-01
; PRIOR APPLICATION NUMBER: 08/412,033
; PRIOR FILING DATE: 1995-03-28
; PRIOR APPLICATION NUMBER: 08/276,164
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/293,347
; PRIOR FILING DATE: 1994-08-19
; PRIOR APPLICATION NUMBER: 08/413,793
; PRIOR FILING DATE: 1995-03-30
; PRIOR APPLICATION NUMBER: 08/303,241
; PRIOR FILING DATE: 1994-09-07
; PRIOR APPLICATION NUMBER: 08/323,523
; PRIOR FILING DATE: 1994-10-14
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; PRIOR FILING DATE: 1995-06-09
; PRIOR APPLICATION NUMBER: 08/320,011
; PRIOR FILING DATE: 1994-10-05
; PRIOR APPLICATION NUMBER: 08/440,743
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; PRIOR FILING DATE: 1995-02-23
; PRIOR APPLICATION NUMBER: 08/494,619
; PRIOR FILING DATE: 1995-06-23
; PRIOR APPLICATION NUMBER: 08/972,819
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 08/385,268
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; PRIOR APPLICATION NUMBER: 08/964,263
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; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/446,910
; PRIOR FILING DATE: 1995-05-22
; PRIOR APPLICATION NUMBER: 08/429,361
; PRIOR FILING DATE: 1995-04-26
; PRIOR APPLICATION NUMBER: 08/440,817
; PRIOR FILING DATE: 1995-05-15
; PRIOR APPLICATION NUMBER: 60/000,275
; PRIOR FILING DATE: 1995-06-16
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; PRIOR FILING DATE: 1996-06-14
; PRIOR APPLICATION NUMBER: 60/000,744
; PRIOR FILING DATE: 1995-06-30
; PRIOR APPLICATION NUMBER: 08/672,741
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 60/001,754
; PRIOR FILING DATE: 1995-08-01
; PRIOR APPLICATION NUMBER: 08/688,870
; PRIOR FILING DATE: 1996-07-31
; PRIOR APPLICATION NUMBER: 60/004,416
; PRIOR FILING DATE: 1995-09-28
; PRIOR APPLICATION NUMBER: 60/004,697
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; PRIOR APPLICATION NUMBER: 08/725,587
; PRIOR FILING DATE: 1996-10-03
; PRIOR APPLICATION NUMBER: 60/005,175
; PRIOR FILING DATE: 1995-10-02
; PRIOR APPLICATION NUMBER: 08/725,863
; PRIOR FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: 60/004,810
; PRIOR FILING DATE: 1995-10-02
; PRIOR APPLICATION NUMBER: 08/724,751
; PRIOR FILING DATE: 1996-10-02
; PRIOR APPLICATION NUMBER: 60/006,111
; PRIOR FILING DATE: 1995-10-24
; PRIOR APPLICATION NUMBER: 08/992,868
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; PRIOR APPLICATION NUMBER: 08/734,050
; PRIOR FILING DATE: 1996-10-18
; PRIOR APPLICATION NUMBER: 60/004,490
; PRIOR FILING DATE: 1995-09-29
; PRIOR APPLICATION NUMBER: 08/723,972
; PRIOR FILING DATE: 1996-09-27
; PRIOR APPLICATION NUMBER: 60/004,672
; PRIOR FILING DATE: 1995-10-02
; PRIOR APPLICATION NUMBER: 08/725,029
; PRIOR FILING DATE: 1996-10-02
; PRIOR APPLICATION NUMBER: 60/005,526
; PRIOR FILING DATE: 1995-09-29
; PRIOR APPLICATION NUMBER: 08/722,922
; PRIOR FILING DATE: 1996-09-27
; PRIOR APPLICATION NUMBER: 60/004,809

; PRIOR FILING DATE: 1995-10-02
; PRIOR APPLICATION NUMBER: 08/725,693
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 60/004,674
; PRIOR FILING DATE: 1995-10-02
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; PRIOR FILING DATE: 1996-10-02
; PRIOR APPLICATION NUMBER: 60/004,676
; PRIOR FILING DATE: 1995-10-02
; PRIOR APPLICATION NUMBER: 08/706,766
; PRIOR FILING DATE: 1996-09-27
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; PRIOR FILING DATE: 1995-10-10
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; PRIOR APPLICATION NUMBER: 60/005,197
; PRIOR FILING DATE: 1995-10-10
; PRIOR APPLICATION NUMBER: 08/726,759
; PRIOR FILING DATE: 1996-10-09
; PRIOR APPLICATION NUMBER: 60/005,008
; PRIOR FILING DATE: 1995-10-10
; PRIOR APPLICATION NUMBER: 08/727,737
; PRIOR FILING DATE: 1996-10-08

Query Match 92.0%; Score 18.4; DB 20; Length 153;
Best Local Similarity 95.0%; Pred. No. 7.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 GGTGTGCGGGGCCTGGTGCC 20
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Db      43 GGTGTCCGGGGCCTGGTGCC 24
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RESULT 14
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; Sequence 823, Application US/09533806
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ISOMERASES
; FILE REFERENCE: PD-1005 CIP
; CURRENT APPLICATION NUMBER: US/09/533,806
; CURRENT FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 07/916,491
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; PRIOR APPLICATION NUMBER: 07/977,780
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; PRIOR APPLICATION NUMBER: 08/100,523
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; PRIOR APPLICATION NUMBER: 09/008,119
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; PRIOR FILING DATE: 1994-04-28
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; PRIOR FILING DATE: 1994-08-26
; PRIOR APPLICATION NUMBER: 08/221,531
; PRIOR FILING DATE: 1994-02-02
; PRIOR APPLICATION NUMBER: 08/435,761
; PRIOR FILING DATE: 1995-05-05
; PRIOR APPLICATION NUMBER: 08/194,317
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: 08/222,611
; PRIOR FILING DATE: 1994-03-31
; PRIOR APPLICATION NUMBER: 08/487,829
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/216,595
; PRIOR FILING DATE: 1994-03-22
; PRIOR APPLICATION NUMBER: 08/499,410
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: 08/271,217
; PRIOR FILING DATE: 1994-06-27
; PRIOR APPLICATION NUMBER: 08/521,383
; PRIOR FILING DATE: 1995-08-16
; PRIOR APPLICATION NUMBER: 08/274,621
; PRIOR FILING DATE: 1994-07-08
; PRIOR APPLICATION NUMBER: 08/413,150
; PRIOR FILING DATE: 1995-03-29
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; PRIOR FILING DATE: 1995-03-30
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; PRIOR FILING DATE: 1995-06-09
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; PRIOR FILING DATE: 1994-10-05
; PRIOR APPLICATION NUMBER: 08/440,743
; PRIOR FILING DATE: 1995-05-12
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; PRIOR FILING DATE: 1994-11-04
; PRIOR APPLICATION NUMBER: 08/369,881
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; PRIOR APPLICATION NUMBER: 08/393,220
; PRIOR FILING DATE: 1995-02-23
; PRIOR APPLICATION NUMBER: 08/494,619
; PRIOR FILING DATE: 1995-06-23
; PRIOR APPLICATION NUMBER: 08/972,819
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 08/385,268
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: 08/964,263
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; PRIOR APPLICATION NUMBER: 08/964,265
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;  PRIOR FILING DATE:       1995-03-21
;  PRIOR APPLICATION NUMBER:       08/413,151
;  PRIOR FILING DATE:       1995-03-29
;  PRIOR APPLICATION NUMBER:       08/502,242
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;  PRIOR FILING DATE:       1995-08-01
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;  PRIOR FILING DATE:       1996-07-31
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;  PRIOR FILING DATE:       1995-10-03
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;  PRIOR FILING DATE:       1996-10-03
;  PRIOR APPLICATION NUMBER:       60/005,175
;  PRIOR FILING DATE:       1995-10-02
;  PRIOR APPLICATION NUMBER:       08/725,863
;  PRIOR FILING DATE:       1996-10-04
;  PRIOR APPLICATION NUMBER:       60/004,810
;  PRIOR FILING DATE:       1995-10-02
;  PRIOR APPLICATION NUMBER:       08/724,751
;  PRIOR FILING DATE:       1996-10-02
;  PRIOR APPLICATION NUMBER:       60/006,111
;  PRIOR FILING DATE:       1995-10-24
;  PRIOR APPLICATION NUMBER:       08/992,868
;  PRIOR FILING DATE:       1997-12-11
;  PRIOR APPLICATION NUMBER:       08/734,050
;  PRIOR FILING DATE:       1996-10-18
;  PRIOR APPLICATION NUMBER:       60/004,490
;  PRIOR FILING DATE:       1995-09-29
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;  PRIOR FILING DATE:       1995-10-02
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;  PRIOR FILING DATE:       1996-10-02
;  PRIOR APPLICATION NUMBER:       60/005,526
;  PRIOR FILING DATE:       1995-09-29
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;  PRIOR FILING DATE:       1995-10-02
;  PRIOR APPLICATION NUMBER:       08/725,693
;  PRIOR FILING DATE:       1996-09-30
;  PRIOR APPLICATION NUMBER:       60/004,674
;  PRIOR FILING DATE:       1995-10-02
;  PRIOR APPLICATION NUMBER:       08/731,034
;  PRIOR FILING DATE:       1996-10-02
;  PRIOR APPLICATION NUMBER:       60/004,676
;  PRIOR FILING DATE:       1995-10-02
;  PRIOR APPLICATION NUMBER:       08/706,766
;  PRIOR FILING DATE:       1996-09-27
;  PRIOR APPLICATION NUMBER:       60/005,023
;  PRIOR FILING DATE:       1995-10-10
;  PRIOR APPLICATION NUMBER:       08/727,870
;  PRIOR FILING DATE:       1996-10-09
;  PRIOR APPLICATION NUMBER:       60/005,197
;  PRIOR FILING DATE:       1995-10-10
;  PRIOR APPLICATION NUMBER:       08/726,759
;  PRIOR FILING DATE:       1996-10-09
;  PRIOR APPLICATION NUMBER:       60/005,008
;  PRIOR FILING DATE:       1995-10-10
;  PRIOR APPLICATION NUMBER:       08/727,737
;  PRIOR FILING DATE:       1996-10-08

  Query Match             92.0%;  Score 18.4;  DB 20;  Length 171;
  Best Local Similarity   95.0%;  Pred. No. 7.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db      30 GGTGTCCGGGGCCTGGTGCC 11


RESULT  15
US-60-023-278-2937/c
; Sequence 2937, Application US/60023278
;  GENERAL INFORMATION:
;    APPLICANT:  Gooding, Douglas H.
;    APPLICANT:  Stuve, Laura L.
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Ito, Laura Y.
;    APPLICANT:  Akerblom, Ingrid E.
;    APPLICANT:  Delegeane, Angelo M.
;    APPLICANT:  Naughton, Rebecca E.
;    APPLICANT:  Klingler, Tod M.
;    TITLE OF INVENTION:  POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
;    TITLE OF INVENTION:  HUMAN UTERUS
;    NUMBER OF SEQUENCES:  3768
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/023,278
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CERRONE, MICHAEL C., Ph.D.
;      REGISTRATION NUMBER:  39132
;      REFERENCE/DOCKET NUMBER:  PD-0211P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 855-0555
;      TELEFAX:  (415) 845-4166
;  INFORMATION FOR SEQ ID NO:  2937:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  171 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      CLONE:  1638235
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US-60-023-278-2937

Query Match 92.0%; Score 18.4; DB 34; Length 171;
Best Local Similarity 95.0%; Pred. No. 7.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      30 GGTGTCCGGGGCCTGGTGCC 11
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Search completed: April 20, 2001, 03:21:21
Job time: 14168 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:15:28 ; Search time 101.94 Seconds
(without alignments)
27.149 Million cell updates/sec

Title: US-09-016-464-16
Perfect score: 20
Sequence: 1 GGTGTGCGGGGCCTGGTGCC 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 46985 seqs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	5	US-09-543-679A-1046	Sequence 1046, Ap
	2	20	100.0	180	5	US-09-543-679A-1725	Sequence 1725, Ap
c	3	20	100.0	827	5	US-09-543-679A-2970	Sequence 2970, Ap
	4	20	100.0	6225	5	US-09-543-679A-2410	Sequence 2410, Ap
	5	20	100.0	35459	5	US-09-543-679A-3003	Sequence 3003, Ap
	6	15.8	79.0	480	5	US-09-739-449-7833	Sequence 7833, Ap
	7	15.8	79.0	803	5	US-09-739-449-71	Sequence 71, Appl
c	8	15.8	79.0	3750	6	US-60-248-505-1443	Sequence 1443, Ap
	9	15.8	79.0	4069	6	US-60-248-505-1852	Sequence 1852, Ap
	10	15.8	79.0	143551	5	US-09-739-449-203	Sequence 203, App
c	11	15.8	79.0	144245	6	US-60-248-505-111	Sequence 111, App
c	12	15.8	79.0	156975	6	US-60-248-505-520	Sequence 520, App
	13	15.4	77.0	493	4	US-08-276-163D-13715	Sequence 13715, A
	14	15.2	76.0	317	4	US-08-276-163D-14916	Sequence 14916, A
	15	15.2	76.0	494	4	US-08-276-163D-2027	Sequence 2027, Ap
	16	15.2	76.0	497	4	US-08-276-163D-8557	Sequence 8557, Ap
c	17	15.2	76.0	501	4	US-08-276-163D-11669	Sequence 11669, A
c	18	15.2	76.0	1378	5	US-09-423-844-262	Sequence 262, App
c	19	15.2	76.0	22081	6	US-60-248-505-38	Sequence 38, Appl
	20	15.2	76.0	30601	6	US-60-248-505-129	Sequence 129, App
c	21	14.8	74.0	404	5	US-09-813-206-253	Sequence 253, App
c	22	14.8	74.0	477	4	US-08-276-163D-2699	Sequence 2699, Ap
	23	14.8	74.0	498	4	US-08-276-163D-14118	Sequence 14118, A
c	24	14.8	74.0	1089	5	US-09-739-449-875	Sequence 875, App
c	25	14.8	74.0	1112	5	US-09-739-449-1516	Sequence 1516, Ap
c	26	14.8	74.0	19410	6	US-60-248-505-50	Sequence 50, Appl
	27	14.8	74.0	449171	6	US-60-248-505-42	Sequence 42, Appl
	28	14.4	72.0	504	4	US-08-276-163D-191	Sequence 191, App
c	29	14.2	71.0	229	5	US-09-442-384-134	Sequence 134, App
	30	14.2	71.0	480	4	US-08-276-163D-8656	Sequence 8656, Ap
	31	14.2	71.0	486	4	US-08-276-163D-7821	Sequence 7821, Ap
	32	14.2	71.0	882	5	US-09-739-449-4672	Sequence 4672, Ap
c	33	14.2	71.0	921	5	US-09-739-449-1357	Sequence 1357, Ap
	34	14.2	71.0	1671	1	PCT-US01-01351-340	Sequence 340, App
	35	14.2	71.0	1671	1	PCT-US01-01351-341	Sequence 341, App
	36	14.2	71.0	1671	1	PCT-US01-01351-342	Sequence 342, App
c	37	14.2	71.0	10046	1	PCT-US01-01351-458	Sequence 458, App
c	38	14.2	71.0	13491	6	US-60-248-505-337	Sequence 337, App
c	39	14.2	71.0	14780	6	US-60-248-505-130	Sequence 130, App
c	40	14.2	71.0	18676	6	US-60-248-505-428	Sequence 428, App
	41	14.2	71.0	18772	1	PCT-US01-01315-63	Sequence 63, Appl
	42	14.2	71.0	19650	5	US-09-819-989-3	Sequence 3, Appli
c	43	14.2	71.0	21287	6	US-60-248-505-415	Sequence 415, App
	44	14.2	71.0	27355	6	US-60-248-505-643	Sequence 643, App
	45	14.2	71.0	27785	6	US-60-248-505-284	Sequence 284, App

ALIGNMENTS

```
RESULT   1
US-09-543-679A-1046
; Sequence 1046, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1046:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1046:
US-09-543-679A-1046


  Query Match             100.0%;  Score 20;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy      1 GGTGTGCGGGGCCTGGTGCC 20
          ||||||||||||||||||||
Db      1 GGTGTGCGGGGCCTGGTGCC 20


RESULT   2
US-09-543-679A-1725
; Sequence 1725, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1725:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1725:
US-09-543-679A-1725


  Query Match             100.0%;  Score 20;  DB 5;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGTGTGCGGGGCCTGGTGCC 20
          ||||||||||||||||||||
Db      1 GGTGTGCGGGGCCTGGTGCC 20


RESULT   3
US-09-543-679A-2970/c
; Sequence 2970, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2970:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 827 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2970:
US-09-543-679A-2970


  Query Match             100.0%;  Score 20;  DB 5;  Length 827;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGTGTGCGGGGCCTGGTGCC 20
          ||||||||||||||||||||
Db     68 GGTGTGCGGGGCCTGGTGCC 49


RESULT   4
US-09-543-679A-2410
; Sequence 2410, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
```

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;             FILING DATE: 1998-08-03
;          ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;          TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;    INFORMATION FOR SEQ ID NO: 2410:
;          SEQUENCE CHARACTERISTICS:
;             LENGTH: 6225 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;          SEQUENCE DESCRIPTION: SEQ ID NO: 2410:
US-09-543-679A-2410


  Query Match             100.0%;  Score 20;  DB 5;  Length 6225;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGTGTGCGGGGCCTGGTGCC 20
          ||||||||||||||||||||
Db    133 GGTGTGCGGGGCCTGGTGCC 152


RESULT   5
US-09-543-679A-3003
; Sequence 3003, Application US/09543679A
;   GENERAL INFORMATION:
;          APPLICANT: NYCE, Jonathan W.
;          TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                              COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                              OF AIRWAY DISORDERS ASSOCIATED WITH
;                              BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;          NUMBER OF SEQUENCES: 3111
;          CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;          COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;          CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;          PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;          ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;          TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;    INFORMATION FOR SEQ ID NO: 3003:
;          SEQUENCE CHARACTERISTICS:
;             LENGTH: 35459 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;          SEQUENCE DESCRIPTION: SEQ ID NO: 3003:
US-09-543-679A-3003


  Query Match             100.0%;  Score 20;  DB 5;  Length 35459;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGTGTGCGGGGCCTGGTGCC 20
          ||||||||||||||||||||
Db    133 GGTGTGCGGGGCCTGGTGCC 152


RESULT   6
US-09-739-449-7833
; Sequence 7833, Application US/09739449
; GENERAL INFORMATION:
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15490)C
;  CURRENT APPLICATION NUMBER: US/09/739,449
;  CURRENT FILING DATE:  2000-12-19
;  PRIOR APPLICATION NUMBER: US 09/514,000
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 7833
;   LENGTH: 480
;   TYPE: DNA
;   ORGANISM: Agrobacterium tumefaciens
US-09-739-449-7833


  Query Match             79.0%;  Score 15.8;  DB 5;  Length 480;
  Best Local Similarity   89.5%;  Pred. No. 97;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGTGTGCGGGGCCTGGTGC 19
          || |||||||||| |||||
Db    208 ggcgtgcggggccgggtgc 226


RESULT   7
US-09-739-449-71
; Sequence 71, Application US/09739449
; GENERAL INFORMATION:
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15490)C
;  CURRENT APPLICATION NUMBER: US/09/739,449
;  CURRENT FILING DATE:  2000-12-19
;  PRIOR APPLICATION NUMBER: US 09/514,000
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 71
;   LENGTH: 803
;   TYPE: DNA
;   ORGANISM: Agrobacterium tumefaciens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(803)
;   OTHER INFORMATION: unsure at all n locations
US-09-739-449-71


  Query Match             79.0%;  Score 15.8;  DB 5;  Length 803;
  Best Local Similarity   89.5%;  Pred. No. 92;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGTGTGCGGGGCCTGGTGC 19
          || |||||||||||| ||
Db    105 ggggtgcggggcctggggc 123
```

```
RESULT   8
US-60-248-505-1443/c
; Sequence 1443, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: cl000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1443
;   LENGTH: 3750
;   TYPE: DNA
;   ORGANISM: Human
US-60-248-505-1443


  Query Match             79.0%;  Score 15.8;  DB 6;  Length 3750;
  Best Local Similarity   89.5%;  Pred. No. 78;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GTGTGCGGGGCCTGGTGCC 20
           ||| |||||||||||| |||
Db    1722 GTGGGCGGGGCCTGGAGCC 1704


RESULT   9
US-60-248-505-1852
; Sequence 1852, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: cl000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1852
;   LENGTH: 4069
;   TYPE: DNA
;   ORGANISM: Human
US-60-248-505-1852


  Query Match             79.0%;  Score 15.8;  DB 6;  Length 4069;
  Best Local Similarity   89.5%;  Pred. No. 77;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GTGTGCGGGGCCTGGTGCC 20
           ||| |||||||||||| |||
Db    3345 gtgggcggggcctggagcc 3363


RESULT  10
US-09-739-449-203
; Sequence 203, Application US/09739449
; GENERAL INFORMATION:
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15490)C
;  CURRENT APPLICATION NUMBER: US/09/739,449
;  CURRENT FILING DATE:  2000-12-19
;  PRIOR APPLICATION NUMBER: US 09/514,000
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 203
;   LENGTH: 143551
;   TYPE: DNA
;   ORGANISM: Agrobacterium tumefaciens
US-09-739-449-203


  Query Match             79.0%;  Score 15.8;  DB 5;  Length 143551;
  Best Local Similarity   89.5%;  Pred. No. 51;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GGTGTGCGGGGCCTGGTGC 19
           || |||||||||| |||||
Db   42073 ggcgtgcggggccgggtgc 42091


RESULT  11
US-60-248-505-111/c
; Sequence 111, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: cl000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
;   LENGTH: 144245
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(144245)
;   OTHER INFORMATION: n = A,T,C or G
US-60-248-505-111


  Query Match             79.0%;  Score 15.8;  DB 6;  Length 144245;
  Best Local Similarity   89.5%;  Pred. No. 51;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GTGTGCGGGGCCTGGTGCC 20
           ||| |||||||||||| |||
Db   91555 GTGGGCGGGGCCTGGAGCC 91537


RESULT  12
US-60-248-505-520/c
; Sequence 520, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: cl000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 520
;   LENGTH: 156975
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(156975)
;   OTHER INFORMATION: n = A,T,C or G
US-60-248-505-520


  Query Match             79.0%;  Score 15.8;  DB 6;  Length 156975;
  Best Local Similarity   89.5%;  Pred. No. 51;
```

```
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GTGTGCGGGGCCTGGTGCC 20
           ||| |||||||||| |||
Db   55003 GTGGGCGGGGCCTGGAGCC 54985


RESULT  13
US-08-276-163D-13715
; Sequence 13715, Application US/08276163D
; GENERAL INFORMATION:
;  APPLICANT: Adams, et. al.
;  TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
;  FILE REFERENCE: PO14
;  CURRENT APPLICATION NUMBER: US/08/276,163D
;  CURRENT FILING DATE:  1994-07-15
;  NUMBER OF SEQ ID NOS: 15314
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13715
;   LENGTH: 493
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (2)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (10)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (84)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (268)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (280)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (294)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (296)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (310)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (311)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (319)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (322)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (323)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (327)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (329)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (333)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (342)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (345)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (346)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (350)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (355)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (359)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (364)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (373)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (374)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (375)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (378)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (382)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (388)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (389)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (392)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (398)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (402)
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;   NAME/KEY: misc feature
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;   NAME/KEY: misc feature
;   LOCATION: (421)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (424)
;   OTHER INFORMATION: n equals a,t,g, or c
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;   NAME/KEY: misc feature
;   LOCATION: (426)
;   OTHER INFORMATION: n equals a,t,g, or c
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;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (461)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (463)
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;   LOCATION: (478)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (482)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (491)
;   OTHER INFORMATION: n equals a,t,g, or c
US-08-276-163D-13715


  Query Match             77.0%;  Score 15.4;  DB 4;  Length 493;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 TGTGCGGGGCCTGGTGCC 20
          | |||||||||| |||||
Db    432 tttgcggggcctngtgcc 449


RESULT  14
US-08-276-163D-14916
; Sequence 14916, Application US/08276163D
; GENERAL INFORMATION:
;  APPLICANT: Adams, et. al.
;  TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
;  FILE REFERENCE: PO14
;  CURRENT APPLICATION NUMBER: US/08/276,163D
;  CURRENT FILING DATE:  1994-07-15
;  NUMBER OF SEQ ID NOS: 15314
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14916
;   LENGTH: 317
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (159)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (197)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (233)
;   OTHER INFORMATION: n equals a,t,g, or c
US-08-276-163D-14916


  Query Match             76.0%;  Score 15.2;  DB 4;  Length 317;
  Best Local Similarity   85.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GGTGTGCGGGGCCTGGTGCC 20
          ||||||| |||| ||||| |
Db    169 ggtgtgctgggcatggtggc 188


RESULT  15
US-08-276-163D-2027
; Sequence 2027, Application US/08276163D
; GENERAL INFORMATION:
;  APPLICANT: Adams, et. al.
;  TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
;  FILE REFERENCE: PO14
;  CURRENT APPLICATION NUMBER: US/08/276,163D
;  CURRENT FILING DATE:  1994-07-15
;  NUMBER OF SEQ ID NOS: 15314
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2027
;   LENGTH: 494
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (198)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (300)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (307)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (374)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (393)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (398)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (408)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (427)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (429)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (453)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (455)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (464)
;   OTHER INFORMATION: n equals a,t,g, or c
US-08-276-163D-2027


  Query Match             76.0%;  Score 15.2;  DB 4;  Length 494;
  Best Local Similarity   85.0%;  Pred. No. 1.7e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GGTGTGCGGGGCCTGGTGCC 20
          || || ||||||| ||||||
Db     50 ggagtacggggccaggtgcc 69


Search completed: April 20, 2001, 00:15:36
Job time: 9473 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:00:22 ; Search time 2028.86 Seconds
(without alignments)
57.668 Million cell updates/sec

Title: US-09-016-464-17
Perfect score: 19
Sequence: 1 GGGCGCGGGCGAGCATCGC 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
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8: gb_ov:*
9: gb_pat1:*
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26: em_htg_hum5:*
27: em_htg_hum6:*
28: em_htg_hum7:*
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30: em_htg_inv1:*
31: em_htg_inv2:*
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33: em_htg_rod:*
34: em_hum1:*
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54: gb_sts2:*
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56: gb_sy:*
57: gb_un:*
58: gb_vi1:*
59: gb_vi2:*
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61: gb_htg2:*
62: gb_htg3:*
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67: gb_htg8:*
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69: gb_htg10:*
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86: gb_pr2:*
87: gb_pr3:*
88: gb_pr4:*
89: gb_pr5:*
90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_ro1:*
95: gb_ro2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	19	100.0	23	9	AR106710	AR106710 Sequence
c	2	19	100.0	23	10	I24358	I24358 Sequence 8
c	3	19	100.0	340	54	G63807	G63807 COX2 Exon1
c	4	19	100.0	1400	88	AF276953	AF276953 Homo sapi
c	5	19	100.0	1834	9	AR055229	AR055229 Sequence
c	6	19	100.0	1834	9	AR055235	AR055235 Sequence
c	7	19	100.0	3362	93	HUMENDOSYN	L15326 Human endop
c	8	19	100.0	3387	9	AR029278	AR029278 Sequence
c	9	19	100.0	3387	10	I24360	I24360 Sequence 11
c	10	19	100.0	3387	93	HUMCYCLOX	M90100 Homo sapien
c	11	19	100.0	10997	93	HUMPTGS2	D28235 Human PTGS2

	12	19	100.0	84412	92	HS973M2	AL033533 Human DNA
c	13	17.4	91.6	654	45	E10546	E10546 DNA encodin
c	14	17.4	91.6	654	45	E10547	E10547 DNA encodin
c	15	17.4	91.6	2763	94	CPCOX2	Y07896 C.porcellus
c	16	17.4	91.6	3314	7	U97696	U97696 Oryctolagus
c	17	17.4	91.6	11702	1	AE001916	AE001916 Deinococc
	18	17.4	91.6	37931	3	SCD10	AL359988 Streptomy
c	19	17.4	91.6	73934	1	AB039932	AB039932 Agrobacte
	20	17.4	91.6	133965	88	AF064861	AF064861 Homo sapi
c	21	17.4	91.6	213732	1	AE001862	AE001862 Deinococc
c	22	17.4	91.6	217594	2	AP002086	AP002086 Agrobacte
	23	17.4	91.6	340000	91	HS21C079	AL163279 Homo sapi
	24	17	89.5	18	9	AR029265	AR029265 Sequence
c	25	17	89.5	3387	9	AR106720	AR106720 Sequence
c	26	17	89.5	3398	7	AF027334	AF027334 Equus cab
c	27	17	89.5	8479	7	AF027335	AF027335 Equus cab
c	28	17	89.5	9453	93	HSU04636	U04636 Human cyclo
c	29	16.4	86.3	1825	7	AF047841	AF047841 Mustela v
c	30	16.4	86.3	2948	3	RHBRTXAB	L01470 Bradyrhizob
c	31	16.4	86.3	3000	2	AVPTSP	Y14681 Azotobacter
c	32	16.4	86.3	3100	2	HSU62676	U62676 Halobacteri
c	33	16.4	86.3	5700	3	RCRNFABCD	Y11913 R.capsulatu
c	34	16.4	86.3	10102	1	AE004712	AE004712 Pseudomon
c	35	16.4	86.3	10483	1	AE001887	AE001887 Deinococc
	36	16.4	86.3	10552	1	AE001989	AE001989 Deinococc
	37	16.4	86.3	10784	1	AE005080	AE005080 Halobacte
	38	16.4	86.3	12092	1	AE004571	AE004571 Pseudomon
	39	16.4	86.3	12480	3	RCRNFG	X72888 R.capsulatu
	40	16.4	86.3	14377	3	SSP277295	AJ277295 Sphingomo
	41	16.4	86.3	22396	3	SCF43	AL136502 Streptomy
c	42	16.4	86.3	34611	3	SCD63A	AL356832 Streptomy
c	43	16.4	86.3	39228	2	MLCB1788	AL008609 Mycobacte
c	44	16.4	86.3	166753	13	AP002866	AP002866 Oryza sat
c	45	16	84.2	41	9	AR106716	AR106716 Sequence

ALIGNMENTS

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RESULT   1
AR106710/c
LOCUS       AR106710        23 bp    DNA             PAT       14-FEB-2001
DEFINITION  Sequence 8 from patent US 6107087.
ACCESSION   AR106710
VERSION     AR106710.1  GI:12821240
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   O'Neill,G.P. and Mancini,J.A.
  TITLE     High level expression of human cyclooxygenase-2
  JOURNAL   Patent: US 6107087-A 8 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
BASE COUNT        1 a      11 c       7 g       4 t
ORIGIN


  Query Match             100.0%;  Score 19;  DB 9;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           |||||||||||||||||||
Db      21 GGGCGCGGGCGAGCATCGC 3


RESULT   2
I24358/c
LOCUS       I24358          23 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 8 from patent US 5543297.
ACCESSION   I24358
VERSION     I24358.1  GI:1604228
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Cromlish,W.A., Kennedy,B.P., O'Neill,G., Vickers,P.J., Wong,E. and
            Mancini,J.A.
  TITLE     Human cyclooxygenase-2 cDNA and assays for evaluating
            cyclooxygenase-2 activity
  JOURNAL   Patent: US 5543297-A 8 06-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
BASE COUNT        1 a      11 c       7 g       4 t
ORIGIN


  Query Match             100.0%;  Score 19;  DB 10;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           |||||||||||||||||||
Db      21 GGGCGCGGGCGAGCATCGC 3


RESULT   3
G63807/c
LOCUS       G63807          340 bp    DNA             STS       20-DEC-1999
DEFINITION  COX2 Exon1 Random genomic STS Homo sapiens STS genomic, sequence
            tagged site.
ACCESSION   G63807
VERSION     G63807.1  GI:6606624
KEYWORDS    STS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Oefner,P.J.
  TITLE     Human random genomic STS survey, unpublished data
  JOURNAL   Unpublished (1999)
COMMENT
            Contact: Peter Oefner
            Stanford Genome Center
            Stanford University
            855 California Ave., Palo Alto, CA 94304, USA
            Tel: 6508121926
            Fax: 6508121975
            Email: Oefner@genome.stanford.edu
            Primer A: TATAAAAAGGAAGGTTCTCTCGGT
            Primer B: AGTCACGTAGCTTCTCTATTCGG
            STS size: 340
            PCR Profile:
            Initial denaturing step of 95 degrees C for 10 min to activate
            AmplTaq Gold (1
            min for AmpliTaq);
            14 cycles of touchdown: 94 degrees C for 20 sec, annealing for 1
            min at 63
            degrees C to
            56 degrees C using decrements of 0.5 degrees C, extension at 72
            degrees C for 1
            min;
            20 cycles at 94 degrees C for 20s, 56 degrees C for 45 sec, 72
            degrees C for 1
            min.
            Protocol:
               Template:        50 ng
               Primer:          each 0.2 uM
               Taq Polymerase:  0.02 units/ul
               Total Vol:       50 ul
```

```
           Buffer:
           MgCl2:     1.5 mM
           KCl:       50 mM
           Tris-HCl:  10 mM
           pH:        8.3
           DMSO:      10 %.
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Random genomic STS"
                     /sex="Male and Female"
     STS             1. .340
     primer_bind     1. .24
     primer_bind     complement(318. .340)
BASE COUNT       63 a    125 c     89 g     63 t
ORIGIN


  Query Match            100.0%;  Score 19;  DB 54;  Length 340;
  Best Local Similarity  100.0%;  Pred. No. 6.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           |||||||||||||||||||
Db     181 GGGCGCGGGCGAGCATCGC 163


RESULT   4
AF276953/c
LOCUS       AF276953     1400 bp    DNA             PRI       16-JUL-2000
DEFINITION  Homo sapiens cyclooxygenase-2 (PTGS2) gene, promoter region and
            partial cds.
ACCESSION   AF276953
VERSION     AF276953.1  GI:9230774
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1400)
  AUTHORS   Lukiw,W.J., Pelaez,R.P., Martinez,J. and Bazan,N.G.
  TITLE     Budesonide epimer R or dexamethasone selectively inhibit
            platelet-activating factor-induced or interleukin 1beta-induced DNA
            binding activity of cis-acting transcription factors and
            cyclooxygenase-2 gene expression in human epidermal keratinocytes
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3914-3919 (1998)
  MEDLINE   98188304
REFERENCE   2  (bases 1 to 1400)
  AUTHORS   Lukiw,W.J. and Bazan,N.G.
  TITLE     Regulatory features of the human cyclooxygenase-2 (COX-2) promoter
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1400)
  AUTHORS   Lukiw,W.J. and Bazan,N.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUN-2000) Neuroscience and Ophthalmology, Louisiana
            State University School of Medicine, 2020 Gravier Street, New
            Orleans, LA 70112-22272, USA
FEATURES             Location/Qualifiers
     source          1. .1400
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1q25.2"
                     /tissue_type="epidermal keratinocytes in primary culture"
     misc_feature    1. .50
                     /gene="PTGS2"
                     /note="potential scaffold/matrix attachment region; S/MAR"
     promoter        1. .1201
                     /gene="PTGS2"
     gene            1. .>1400
                     /gene="PTGS2"
                     /note="COX2"
     protein_bind    263. .269
                     /gene="PTGS2"
                     /note="AP1-like site"
                     /bound_moiety="AP1"
     protein_bind    359. .365
                     /gene="PTGS2"
                     /note="AP1-like site"
                     /bound_moiety="AP1"
     protein_bind    443. .453
                     /gene="PTGS2"
                     /note="GAS-binding"
                     /bound_moiety="STAT1"
     protein_bind    555. .562
                     /gene="PTGS2"
                     /note="SIE-binding"
                     /bound_moiety="STAT3"
     protein_bind    635. .641
                     /gene="PTGS2"
                     /note="AP1-like site"
                     /bound_moiety="AP1"
     protein_bind    748. .768
                     /gene="PTGS2"
                     /bound_moiety="NF-kappaB"
     protein_bind    939. .952
                     /gene="PTGS2"
                     /note="AP2-like site"
                     /bound_moiety="AP2"
     protein_bind    972. .992
                     /gene="PTGS2"
                     /bound_moiety="NF-kappaB"
     protein_bind    1056. .1067
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                     /bound_moiety="AP2"
     protein_bind    1069. .1076
                     /gene="PTGS2"
                     /note="SIE-binding"
                     /bound_moiety="STAT3"
     protein_bind    1078. .1085
                     /gene="PTGS2"
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                     /bound_moiety="STAT3"
     protein_bind    1168. .1178
                     /gene="PTGS2"
                     /note="GAS-binding"
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                     /gene="PTGS2"
     protein_bind    1170. .1173
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                     /bound_moiety="TFIID"
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                     /product="cyclooxygenase-2"
     CDS             1335. .>1400
                     /gene="PTGS2"
                     /EC_number="1.14.99.1"
                     /codon_start=1
                     /product="cyclooxygenase-2"
                     /protein_id="AAF85977.1"
                     /db_xref="GI:9230775"
                     /translation="MLARALLLCAVLXLSHTGEYLA"
     protein_bind    1358. .1365
                     /gene="PTGS2"
                     /note="zif268-binding"
                     /bound_moiety="EGR1"
BASE COUNT      379 a    361 c    337 g    322 t      1 others
ORIGIN


  Query Match            100.0%;  Score 19;  DB 88;  Length 1400;
  Best Local Similarity  100.0%;  Pred. No. 4.1e+02;
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||||||||
Db   1350 GGGCGCGGGCGAGCATCGC 1332


RESULT   5
AR055229/c
LOCUS       AR055229     1834 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 3 from patent US 5837479.
ACCESSION   AR055229
VERSION     AR055229.1  GI:5980806
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1834)
  AUTHORS   Young,D.A., O'Banion,M.K. and Winn,V.D.
  TITLE     Screening assays for inhibitors of mammalian prostaglandin H
            synthase-2
  JOURNAL   Patent: US 5837479-A 3 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .1834
                     /organism="unknown"
BASE COUNT      517 a    441 c    387 g    489 t
ORIGIN


  Query Match           100.0%;  Score 19;  DB 9;  Length 1834;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
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Db     24 GGGCGCGGGCGAGCATCGC 6


RESULT   6
AR055235/c
LOCUS       AR055235     1834 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 14 from patent US 5837479.
ACCESSION   AR055235
VERSION     AR055235.1  GI:5980812
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1834)
  AUTHORS   Young,D.A., O'Banion,M.K. and Winn,V.D.
  TITLE     Screening assays for inhibitors of mammalian prostaglandin H
            synthase-2
  JOURNAL   Patent: US 5837479-A 14 17-NOV-1998;
FEATURES             Location/Qualifiers
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BASE COUNT      517 a    441 c    387 g    489 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 3.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||||||||
Db     24 GGGCGCGGGCGAGCATCGC 6


RESULT   7
HUMENDOSYN/c
LOCUS       HUMENDOSYN   3362 bp    mRNA            PRI       12-JUN-1993
DEFINITION  Human endoperoxide synthase type II mRNA, complete cds.
ACCESSION   L15326
VERSION     L15326.1  GI:291987
KEYWORDS    endoperoxide synthase type II.
SOURCE      Homo sapiens (library: lambda gt11) prostaglandin cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3362)
  AUTHORS   Jones,D.A., Carlton,D.P., McIntyre,T.M., Zimmerman,G.A. and
            Prescott,S.M.
  TITLE     Molecular cloning of human prostaglandin endoperoxide synthase type
            II and demonstration of expression in response to cytokines
  JOURNAL   J. Biol. Chem. 268, 9049-9054 (1993)
  MEDLINE   93232069
FEATURES             Location/Qualifiers
     source          1. .3362
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                     /db_xref="taxon:9606"
                     /cell_line="primary"
                     /cell_type="endothelial"
                     /tissue_type="prostaglandin"
                     /tissue_lib="lambda gt11"
                     /map="Chromosome 1"
     CDS             93. .1907
                     /codon_start=1
                     /product="endoperoxide synthase type II"
                     /protein_id="AAA35803.1"
                     /db_xref="GI:291988"
                     /translation="MLARALLLCAVLALSHTANPCCSHPCQNRGVCMSVGFDQYKCDC
                     TRTGFYGENCSTPEFLTRIKLFLKPTPNTVHYILTHFKGFWNVVNNIPFLRNAIMSYV
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                     NEIVEKLLLRRKFIPDPQGSNMMFAFFAQHFTHQFFKTDHKRGPAFTNGLGHGVDLNH
                     IYGETLARQRKLRLFKDGKMKYQIIDGEMYPPTVKDTQAEMIYPPQVPEHLRFAVGQE
                     VFGLVPGLMMYATIWLREHNRVCDVLKQEHPEWGDEQLFQTSRLILIGETIKIVIEDY
                     VQHLSGYHFKLKFDPELLFNKQFQYQNRIAAEFNTLYHWHPLLPDTFQIHDQKYNYQQ
                     FIYNNSILLEHGITQFVESFTRQIAGRVAGGRNVPPAVQKVSQASTDQSRQMKYQSFN
                     EYRKRFMLKPYESFEELTGEKEMSAELEALYGDIDAVELYPALLVEKPRPDAIFGETM
                     VEVGAPFSLKGLMGNVICSPAYWKPSTFGGEVGFQIINTASIQSLICNNVKGCPFTSF
                     SVPDPELIKTVTINASSSRSGLDDINPTVLLKERSTEL"
BASE COUNT     1000 a    697 c    626 g   1039 t
ORIGIN


  Query Match           100.0%;  Score 19;  DB 93;  Length 3362;
  Best Local Similarity  100.0%;  Pred. No. 3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||||||||
Db    108 GGGCGCGGGCGAGCATCGC 90


RESULT   8
AR029278/c
LOCUS       AR029278     3387 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 29 from patent US 5859229.
ACCESSION   AR029278
VERSION     AR029278.1  GI:5941251
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3387)
  AUTHORS   Kniss,D.A.
  TITLE     Antisense oligonucleotides to suppress eicosanoid formation
  JOURNAL   Patent: US 5859229-A 29 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .3387
                     /organism="unknown"
BASE COUNT     1011 a    712 c    633 g   1031 t
ORIGIN
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  Query Match             100.0%;  Score 19;  DB 9;  Length 3387;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db    113 GGGCGCGGGCGAGCATCGC 95


RESULT   9
I24360/c
LOCUS       I24360       3387 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 11 from patent US 5543297.
ACCESSION   I24360
VERSION     I24360.1  GI:1604230
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3387)
  AUTHORS   Cromlish,W.A., Kennedy,B.P., O'Neill,G., Vickers,P.J., Wong,E. and
            Mancini,J.A.
  TITLE     Human cyclooxygenase-2 cDNA and assays for evaluating
            cyclooxygenase-2 activity
  JOURNAL   Patent: US 5543297-A 11 06-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .3387
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BASE COUNT     1010 a    713 c    633 g   1031 t
ORIGIN


  Query Match             100.0%;  Score 19;  DB 10;  Length 3387;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db    113 GGGCGCGGGCGAGCATCGC 95


RESULT  10
HUMCYCLOX/c
LOCUS       HUMCYCLOX    3387 bp    mRNA            PRI       31-DEC-1994
DEFINITION  Homo sapiens cyclooxygenase-2 (Cox-2) mRNA, complete cds.
ACCESSION   M90100
VERSION     M90100.1  GI:181253
KEYWORDS    cyclooxygenase-2; prostaglandin synthase.
SOURCE      Homo sapiens umbilical vein cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3387)
  AUTHORS   Hla,T. and Neilson,K.
  TITLE     Human cyclooxygenase-2 cDNA
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (16), 7384-7388 (1992)
  MEDLINE   92366465
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="umbilical vein"
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     gene            1. .3387
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                     /gene="Cox-2"
                     /EC_number="1.14.99.1"
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                     /product="cyclooxygenase-2"
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                     VFGLVPGLMMYATIWLREHNRVCDVLKQEHPEWGDEQLFQTSRLILIGETIKIVIEDY
                     VQHLSGYHFKLKFDPELLFNKQFQYQNRIAAEFNTLYHWHPLLPDTFQIHDQKYNYQQ
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                     EYRKRFMLKPYESFEELTGEKEMSAELEALYGDIDAVELYPALLVEKPRPDAIFGETM
                     VEVGAPFSLKGLMGNVICSPAYWKPSTFGGEVGFQIINTASIQSLICNNVKGCPFTSF
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     mat_peptide     149. .1909
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                     /EC_number="1.14.99.1"
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     polyA_signal    3369. .3374
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BASE COUNT     1010 a    712 c    633 g   1032 t
ORIGIN


  Query Match             100.0%;  Score 19;  DB 93;  Length 3387;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db    113 GGGCGCGGGCGAGCATCGC 95


RESULT  11
HUMPTGS2/c
LOCUS       HUMPTGS2    10997 bp    DNA             PRI       14-APR-2000
DEFINITION  Human PTGS2 gene for prostaglandin endoperoxide synthase-2,
            complete cds.
ACCESSION   D28235
VERSION     D28235.1  GI:505116
KEYWORDS    prostaglandin endoperoxide synthase-2.
SOURCE      Homo sapiens Japanese peripheral blood DNA, clone_lib:EMBL3.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Hla,T. and Neilson,K.
  TITLE     Human cyclooxygenase-2 cDNA
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (16), 7384-7388 (1992)
  MEDLINE   92366465
REFERENCE   2  (bases 1 to 10997)
  AUTHORS   Kosaka,T., Miyata,A., Ihara,H., Hara,S., Sugimoto,T., Takeda,O.,
            Takahashi,E. and Tanabe,T.
  TITLE     Characterization of the human gene (PTGS2) encoding
            prostaglandin-endoperoxide synthase 2
  JOURNAL   Eur. J. Biochem. 221 (3), 889-897 (1994)
  MEDLINE   94237153
REFERENCE   3  (bases 1 to 10997)
  AUTHORS   Tanabe,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-FEB-1994) to the DDBJ/EMBL/GenBank databases. Tadashi
            Tanabe, National Cardiovascular Center Research Institute,
            Pharmacology; 5-7-1 Fujishiro-dai, Suita, Osaka 565, JAPAN
            (Tel:06-833-5012(ex.2514), Fax:06-872-7485)
COMMENT     Submitted (19-Feb-1994) to DDBJ by:
            Tadashi Tanabe
            National Cardiovascular Center Research Institute
            5-7-1 Fujishiro-dai, Suita
            Osaka 565
            Japan
            Phone: 06-833-5012 x2514
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     protein_bind    584. .589
                     /bound_moiety="myb"
     misc_signal     734. .739
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     protein_bind    982. .990
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     misc_signal     1121. .1127
                     /note="CRE (cAMP-response element)"
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                     /bound_moiety="PEA-3"
     protein_bind    1421. .1426
                     /bound_moiety="Sp-1"
     protein_bind    1468. .1477
                     /bound_moiety="NF-kappaB"
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     TATA_signal     1660. .1666
     exon            1691. .1876
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                     4570. .4751,5484. .5567,5687. .5933,6215. .6501,7003. .7150,
                     7637. .8046)
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                     7637. .8046)
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                     /protein_id="BAA05698.1"
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                     5484. .5567,5687. .5933,6215. .6501,7003. .7150,7637. .8043)
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     misc_signal     10010. .10014

  Query Match             100.0%;  Score 19;  DB 93;  Length 10997;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db   1840 GGGCGCGGGCGAGCATCGC 1822


RESULT  12
HS973M2
LOCUS       HS973M2     84412 bp    DNA             PRI       23-NOV-1999
DEFINITION  Human DNA sequence from clone 973M2 on chromosome 1q24.3-31.1
            Contains prostaglandin-endoperoxide synthase 2 (prostaglandin G/H
            synthase and cyclooxygenase) gene, ESTs, STS, GSSs, complete
            sequence.
ACCESSION   AL033533
VERSION     AL033533.5  GI:4468336
KEYWORDS    HTG; PTGS2.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 84412)
  AUTHORS   Coville,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-1999) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Mar 22, 1999 this sequence version replaced gi:4464261.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            IMPORTANT: This sequence is not the entire insert of clone 973M2.
            It may be shorter because we only sequence overlapping sections
            once, or longer because we arrange for a small overlap between
            neighbouring submissions.
            The true left end of clone dJ936P19 is at 84313 in this sequence.
            This sequence has been finished according to sequence map criteria
            as follows. An attempt is made to resolve all sequencing problems,
            such as compressions and repeats, but not necessarily within known
            annotated human repeat sequence elements (e.g. Alu). Where the
            sequence is ambiguous, there is an annotation using the 'unsure'
            feature key.
            This sequence was generated from part of bacterial clone contigs of
            human chromosome 1, constructed by the Sanger Centre Chromosome 1
            Mapping Group. Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr1
            973M2 is from the library RPCI5 constructed at the Roswell Park
            Cancer Institute by the group of Pieter de Jong. For further
            details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.

FEATURES            Location/Qualifiers
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                    /note="69 copies 3 mer aag 85% conserved"
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     repeat_region  2631. .3236
                    /note="MLT2D repeat: matches 1. .553 of consensus"
     repeat_region  3237. .3384
                    /note="L2 repeat: matches 826. .971 of consensus"
     repeat_region  3558. .3687
                    /note="MLT1C repeat: matches 344. .466 of consensus"
     repeat_region  3688. .4392
                    /note="LTR8 repeat: matches 1. .691 of consensus"
     repeat_region  4393. .4699
                    /note="MLT1C repeat: matches 7. .344 of consensus"
     repeat_region  4757. .4848
                    /note="MIR repeat: matches 164. .257 of consensus"
     repeat_region  5535. .5677
                    /note="MLT1I repeat: matches 129. .276 of consensus"
     repeat_region  5909. .6211
                    /note="AluSq repeat: matches 1. .307 of consensus"
     repeat_region  6521. .6798
                    /note="AluSx repeat: matches 1. .297 of consensus"
     repeat_region  7309. .7593
                    /note="L2 repeat: matches 2258. .2525 of consensus"
     repeat_region  7690. .8469
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     repeat_region  8465. .13709
                    /note="L1PA2 repeat: matches 900. .6146 of consensus"
     repeat_region  13912. .14149
                    /note="L2 repeat: matches 1592. .1831 of consensus"
     repeat_region  14537. .14653
                    /note="L1MC1 repeat: matches 6070. .6187 of consensus"
     repeat_region  14658. .14797
                    /note="L1MC1 repeat: matches 6183. .6320 of consensus"
     repeat_region  14822. .15122
                    /note="AluYb8 repeat: matches 1. .308 of consensus"
     repeat_region  15632. .15782
                    /note="LTR35 repeat: matches 454. .613 of consensus"
     repeat_region  16610. .16900
                    /note="AluJo repeat: matches 3. .296 of consensus"
     repeat_region  17460. .17755
                    /note="AluSx repeat: matches 1. .298 of consensus"
     misc_feature   complement(17729. .>18136)
                    /note="match: GSS AQ027623 clone 2322P16"
     repeat_region  18539. .18848
                    /note="AluSg repeat: matches 1. .307 of consensus"
     repeat_region  19806. .19905
                    /note="MLT1C repeat: matches 1. .103 of consensus"
     repeat_region  19906. .20214
                    /note="AluSq repeat: matches 1. .313 of consensus"
     repeat_region  20215. .20370
                    /note="MLT1C repeat: matches 103. .263 of consensus"
     repeat_region  20371. .20603
                    /note="AluSg repeat: matches 43. .283 of consensus"
     repeat_region  20604. .20828
                    /note="MLT1C repeat: matches 263. .466 of consensus"
     repeat_region  21334. .21461
                    /note="L2 repeat: matches 1435. .1567 of consensus"
     repeat_region  22095. .22621
```

```
                     /note="LTR9 repeat: matches 12. .512 of consensus"
     repeat_region   22640. .22769
                     /note="65 copies 2 mer tt 69% conserved"
     repeat_region   22658. .22745
                     /note="4 copies 22 mer 78% conserved"
     repeat_region   22772. .22824
                     /note="LTR9 repeat: matches 450. .502 of consensus"
     repeat_region   22825. .23133
                     /note="AluSx repeat: matches 1. .312 of consensus"
     repeat_region   23134. .23263
                     /note="LTR9 repeat: matches 502. .625 of consensus"
     repeat_region   23857. .24371
                     /note="L2 repeat: matches 707. .1206 of consensus"
     repeat_region   24372. .24493
                     /note="FLAM_C repeat: matches 2. .123 of consensus"
     repeat_region   24494. .24764
                     /note="L2 repeat: matches 433. .707 of consensus"
     repeat_region   24786. .25086
                     /note="AluSc repeat: matches 3. .308 of consensus"
     repeat_region   25087. .25154
                     /note="34 copies 2 mer aa 74% conserved"
     repeat_region   25175. .25369
                     /note="L2 repeat: matches 173. .403 of consensus"
     repeat_region   25391. .25673
                     /note="AluSx repeat: matches 2. .309 of consensus"
     repeat_region   25737. .25825
                     /note="L2 repeat: matches 2571. .2644 of consensus"
     repeat_region   26065. .26216
                     /note="AluSg/x repeat: matches 177. .312 of consensus"
     repeat_region   26650. .26946
                     /note="AluY repeat: matches 1. .296 of consensus"
     repeat_region   27162. .27764
                     /note="L1MD2 repeat: matches 5731. .6333 of consensus"
     repeat_region   28181. .28492
                     /note="AluY repeat: matches 1. .311 of consensus"
     repeat_region   28607. .28733
                     /note="L2 repeat: matches 2553. .2676 of consensus"
     repeat_region   28770. .29111
                     /note="L2 repeat: matches 2089. .2411 of consensus"
     misc_feature    complement(29157. .29553)
                     /note="match: GSS AQ004513 clone 2294C15"
     repeat_region   29185. .29333
                     /note="MIR repeat: matches 10. .159 of consensus"
     misc_feature    complement(29271. .29626)
                     /note="match: GSS AQ005004 clone 2294D2"
     misc_feature    complement(29291. .29581)
                     /note="match: GSS AQ006900 clone 2294C20"
     misc_feature    complement(29629. .29808)
                     /note="match: AL009785 chromosome 1 HindIII fragment"
     repeat_region   30165. .30466
                     /note="L2 repeat: matches 2116. .2405 of consensus"
     repeat_region   30467. .30888
                     /note="MSTA repeat: matches 1. .426 of consensus"
     repeat_region   30889. .31001
                     /note="L2 repeat: matches 2405. .2553 of consensus"
     repeat_region   31002. .31276
                     /note="AluSp repeat: matches 37. .313 of consensus"
     repeat_region   31277. .31303
                     /note="L2 repeat: matches 2553. .2578 of consensus"
     prim_transcript <31738. .33230
                     /note="match: multiple ESTs; match: 3' EST T63799 clone
                     81383; Paired with EST T63823 matching this clone; match:
                     5' EST T63823 clone 81383; Paired with EST T63799 matching
                     this clone"
     repeat_region   31847. .32100
                     /note="L1MA9 repeat: matches 6028. .6292 of consensus"
     repeat_region   32121. .32273
                     /note="L1PA4 repeat: matches 5995. .6146 of consensus"
     repeat_region   32281. .32356
                     /note="38 copies 2 mer ta 68% conserved"
     repeat_region   33919. .34214
                     /note="L1MC1 repeat: matches 5926. .6243 of consensus"
     repeat_region   34262. .34386
                     /note="MLT2E repeat: matches 223. .347 of consensus"
     repeat_region   34377. .34425
                     /note="MLT2FB repeat: matches 267. .315 of consensus"
     repeat_region   34426. .34741
                     /note="AluSg repeat: matches 1. .310 of consensus"
     repeat_region   34742. .34769
                     /note="MLT2FB repeat: matches 240. .267 of consensus"
     repeat_region   34770. .35121
                     /note="MLT1A1 repeat: matches 1. .364 of consensus"
     repeat_region   35122. .35357
                     /note="MLT2FB repeat: matches 1. .380 of consensus"

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  Best Local Similarity  100.0%;  Pred. No. 96;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           ||||||||||||||||||||
Db   50633 GGGCGCGGGCGAGCATCGC 50651


RESULT  13
E10546/c
ID   E10546     standard; DNA; UNC; 654 BP.
XX
AC   E10546;
XX
SV   E10546.1
XX
DT   08-OCT-1997 (Rel. 52, Created)
DT   02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX
DE   DNA encoding thiamin pyrophosphokinase from Paracoccus denitrificans.
XX
KW   JP 1996009985-A/1.
XX
OS   unidentified
OC   unclassified.
XX
RN   [1]
RP   1-654
RA   Iida A., Teshiba S.;
RT   "PRODUCTION OF THIAMINE DIPHOSPHORIC ACID";
RL   Patent number JP1996009985-A/1, 16-JAN-1996.
RL   KYOWA HAKKO KOGYO CO LTD.
XX
CC   OS   Paracoccus denitrificans
CC   PN   JP 1996009985-A/1
CC   PD   16-JAN-1996
CC   PF   01-JUL-1994 JP 1994150847
CC   PI   IIDA AKIHIRO, TESHIBA SADAO
CC   PC   C12P17/16,C12N1/21,C12N15/09//C12N9/12,(C12P17/16,C12R1:19),
CC   PC   (C12N1/21,
CC   PC   C12R1:19),(C12N15/09,C12R1:01);
CC   CC   strandedness: Double;
CC   CC   topology: Linear;
CC   CC   hypothetical: No;
CC   CC   anti-sense: No;
CC   FH   Key             Location/Qualifiers
CC   FH
CC   FT   source          1. .654
CC   FT                   /organism="Paracoccus denitrificans"
CC   FT                   /strain="ATCC19367"
CC   FT                   /clone="pAI213"
CC   FT   mat_peptide     1. .654
CC   FT                   /product="Thiamin pyrophosphokinase from
CC   FT                   Pracoccus
CC   FT                   denitrificans"
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .654
FT                   /db_xref="taxon:32644"
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FT                   /organism="unidentified"
XX
SQ   Sequence 654 BP; 83 A; 246 C; 218 G; 107 T; 0 other;


  Query Match             91.6%;  Score 17.4;  DB 45;  Length 654;
  Best Local Similarity   94.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           ||||||||||||||| ||||
Db     652 GGGCGCGGGCGAGCGTCGC 634


RESULT  14
E10547/c
ID   E10547     standard; DNA; UNC; 654 BP.
XX
AC   E10547;
XX
SV   E10547.1
XX
DT   08-OCT-1997 (Rel. 52, Created)
DT   02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX
DE   DNA encoding variant thiamin pyrophosphokinase which is hyperexpression
DE   type.
XX
KW   JP 1996009985-A/2.
XX
OS   unidentified
OC   unclassified.
XX
RN   [1]
RP   1-654
RA   Iida A., Teshiba S.;
RT   "PRODUCTION OF THIAMINE DIPHOSPHORIC ACID";
RL   Patent number JP1996009985-A/2, 16-JAN-1996.
RL   KYOWA HAKKO KOGYO CO LTD.
XX
CC   OS   Paracoccus denitrificans
CC   PN   JP 1996009985-A/2
CC   PD   16-JAN-1996
CC   PF   01-JUL-1994 JP 1994150847
CC   PI   IIDA AKIHIRO, TESHIBA SADAO
CC   PC   C12P17/16,C12N1/21,C12N15/09//C12N9/12,(C12P17/16,C12R1:19),
CC   PC   (C12N1/21,
CC   PC   C12R1:19),(C12N15/09,C12R1:01);
CC   CC   strandedness: Double;
CC   CC   topology: Linear;
CC   CC   hypothetical: No;
CC   CC   anti-sense: No;
CC   FH   Key             Location/Qualifiers
CC   FH
CC   FT   source          1. .654
CC   FT                   /organism="Paracoccus denitrificans"
CC   FT                   /strain="ATCC19367"
CC   FT                   /clone="pTPK1"
CC   FT   mat_peptide     1. .654
CC   FT                   /product="Variant thiamin pyrophosphokinase
CC   FT                   which is
CC   FT                   hyperexpression type"
CC   FT   misc_feature    replace(6,"C")
CC   FT                   /note="Natural thiamin pyrophosphokinase from
CC   FT                   Paracoccus
CC   FT                   denitrificans"
CC   FT   misc_feature    replace(9,"G")
CC   FT                   /note="Natural thiamin pyrophosphokinase from
CC   FT                   Paracoccus
CC   FT                   denitrificans"
CC   FT   misc_feature    replace(12,"A")
CC   FT                   /note="Natural thiamin pyrophosphokinase from
CC   FT                   Paracoccus
CC   FT                   denitrificans"
CC   FT   misc_feature    replace(15,"G")
CC   FT                   /note="Natural thiamin pyrophosphokinase from
CC   FT                   Paracoccus
CC   FT                   denitrificans"
CC   FT   misc_feature    replace(18,"C")
CC   FT                   /note="Natural thiamin pyrophosphokinase from
CC   FT                   Paracoccus
CC   FT                   denitrificans"
CC   FT   misc_feature    replace(21,"G")
CC   FT                   /note="Natural thiamin pyrophosphokinase from
CC   FT                   Paracoccus
CC   FT                   denitrificans"
CC   FT   misc_feature    replace(22,"T")
CC   FT                   /note="Natural thiamin pyrophosphokinase from
CC   FT                   Paracoccus
CC   FT                   denitrificans"
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .654
FT                   /db_xref="taxon:32644"
FT                   /organism="unidentified"
XX
SQ   Sequence 654 BP; 84 A; 246 C; 216 G; 108 T; 0 other;


  Query Match             91.6%;  Score 17.4;  DB 45;  Length 654;
  Best Local Similarity   94.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           ||||||||||||||| ||||
Db     652 GGGCGCGGGCGAGCGTCGC 634


RESULT  15
CPCOX2/c
LOCUS       CPCOX2       2763 bp    mRNA            ROD       30-APR-1997
DEFINITION  C.porcellus mRNA for cyclooxygenase-2.
ACCESSION   Y07896
VERSION     Y07896.1  GI:1556389
KEYWORDS    cox2 gene; cyclooxygenase-2.
SOURCE      domestic guinea pig.
  ORGANISM  Cavia porcellus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Bracken,K.E., Elger,W., Jantke,I., Nanninga,A. and Gellersen,B.
  TITLE     Cloning of guinea pig cyclooxygenase-2 and 15-hydroxyprostaglandin
            dehydrogenase complementary deoxyribonucleic acids:
            steroid-modulated gene expression correlates to prostaglandin F2
            alpha secretion in cultured endometrial cells
  JOURNAL   Endocrinology 138 (1), 237-247 (1997)
  MEDLINE   97131952
REFERENCE   2  (bases 1 to 2763)
  AUTHORS   Gellersen,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-1996) B. Gellersen, Inst. for Hormone and
            Fertility Research, Grandweg 64, D- 22529 Hamburg, FRG
FEATURES             Location/Qualifiers
     source          1. .2763
                     /organism="Cavia porcellus"
                     /strain="Durukim Hartley"
                     /sub_strain="HSD:WIN"
                     /db_xref="taxon:10141"
                     /tissue_type="uterus"
                     /clone_lib="Uni-Zap XR"
     gene            15. .1829
                     /gene="COX-2"
     CDS             15. .1829
                     /gene="COX-2"
                     /EC_number="1.14.99.1"
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                     /codon_start=1
                     /product="cyclooxygenase-2"
                     /protein_id="CAA69204.1"
                     /db_xref="GI:1556390"
                     /db_xref="SWISS-PROT:P70682"
                     /translation="MLARALLLCAALALGQAANPCCSNPCQNRGECLSVGFDRYKCDC
                     TRTGYYGENCTTPEFLTRIKLLLKPTPNTVHYILTHFKGVWNIVNNIPFLRNAIMIYV
                     LTSRSHLIDSPPTYNAHYGYKSWEAFSNLSYYTRALPPVADDCPTPMGVKGKKELPDS
                     NEVLEKVLLRRKFIPDPQGTNMMFAFFAQHFTHQFFKSDQKRGPAFTTGLAHGVDLSH
                     IYGETLDRQHKLRLFKDGKMKYQIIDGEMYPPTVKETQVEMMYPPYIPEHARFAVGQE
                     VFGLVPGLMMYATIWLREHNRVCDVLKQEHPEWDDERLFQTSRLILIGETIKIVIEDY
                     VQHLSGYHFKLKFDPELLFNQQFQYQNRIASEFNTLYHWHPLLPDTFQIDDQVYNFQQ
                     FLYNNSILVEHGLTQFVESFTKQIAGRVAGGRNVPLAVQRVAKASIEHSRKMKYQSLN
                     EYRKRFLMKPYTSFEELTGEKEMAAGLEALYGDIDAMELYPALLVEKPRPDAIFGETM
                     VEMGAPFSLKGLMGNPICSPHYWKPSTFGGEVGFQIVNTASIQSLICNNVKGCPVTAF
                     NLPDPQLAKTVTINASASHSRLEDLSPTVLLKGRSTEL"
     polyA_signal    2531. .2536
BASE COUNT      798 a    635 c    589 g    741 t
ORIGIN
```

```
  Query Match             91.6%;  Score 17.4;  DB 94;  Length 2763;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           | ||||||||||||||||||
Db      30 GCGCGCGGGCGAGCATCGC 12
```

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Search completed: April 20, 2001, 00:00:25
Job time: 9502 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:12:55 ; Search time 547.68 Seconds
(without alignments)
20.252 Million cell updates/sec

Title: US-09-016-464-17
Perfect score: 19
Sequence: 1 GGGCGCGGGCGAGCATCGC 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0401:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
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9: /SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
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13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	19	100.0	23	15	Q70997	Primer for 5' end
c	2	19	100.0	23	16	Q89384	COX-2 PCR 5' prime
c	3	19	100.0	429	21	C57690	Arachidonic acid m
c	4	19	100.0	1834	15	Q61790	Sequence of human
c	5	19	100.0	1834	18	T59635	Human prostaglandi
c	6	19	100.0	3387	15	Q71002	Cyclooxygenase-2 c
c	7	19	100.0	3387	16	Q89376	Human cyclooxygena
c	8	19	100.0	3387	21	F21115	Human low adenosin
c	9	19	100.0	3387	21	A34993	Human adenosine re
c	10	19	100.0	15240	21	F21117	Human low adenosin
c	11	19	100.0	15240	21	A34995	Human adenosine re
c	12	17.4	91.6	654	17	T08722	Paracoccus denitri
c	13	17.4	91.6	654	17	T08723	Paracoccus denitri
	14	17	89.5	18	16	Q91482	Human cyclooxygena
c	15	17	89.5	9453	21	F21116	Human low adenosin
c	16	17	89.5	9453	21	A34994	Human adenosine re
c	17	16	84.2	41	16	Q89389	COX-2 oligonucleot
	18	15.8	83.2	19	18	T76115	Human cylcooxygena
	19	15.8	83.2	19	20	X53920	Human cyclooxygena
	20	15.8	83.2	19	20	X53923	Eosinophil derived
	21	15.8	83.2	19	21	F19485	Human prostaglandi
	22	15.8	83.2	19	21	A33363	Low adenosine anti
	23	15.8	83.2	60	18	T76114	Human cyclooxygena
	24	15.8	83.2	60	20	X53922	Human cyclooxygena
	25	15.8	83.2	60	20	X53925	Eosinophil derived
	26	15.8	83.2	60	21	F19487	Human prostaglandi
	27	15.8	83.2	60	21	A33365	Low adenosine anti
	28	15.8	83.2	101	20	X54593	Human cyclooxygena
	29	15.8	83.2	101	21	F20162	Human cyclooxygena
	30	15.8	83.2	101	21	A34040	Human adenosine re
c	31	15.8	83.2	2206	15	Q74445	DNA located 3' of
	32	15.8	83.2	6225	20	X55273	Human enzyme-relat
	33	15.8	83.2	6225	21	F20843	Human multiple tar
	34	15.8	83.2	6225	21	A34721	Human adenosine re
c	35	15.8	83.2	7742	18	T84745	Bordetella pertuss
	36	15.8	83.2	11389	19	V34334	Human glycogenin-2
	37	15.8	83.2	35384	21	F21436	Human enzyme-relat
	38	15.8	83.2	114955	20	X53491	Human adenosine A1
	39	15.4	81.1	764	20	X97734	Extended human sec
	40	15.4	81.1	65632	21	A81502	N. meningitidis pa
c	41	15.4	81.1	349980	21	F21544	Neisseria meningit
c	42	15.4	81.1	1437668	21	A81490	N. meningitidis B
	43	15	78.9	15	16	Q91481	Human cyclooxygena
	44	15	78.9	1312	15	Q73383	Human CCAAT/Enhanc
	45	15	78.9	1312	17	T44325	DNA encoding CCAAT

ALIGNMENTS

RESULT 1
Q70997/c
ID Q70997 standard; cDNA; 23 BP.
XX
AC Q70997;
XX
DT 27-FEB-1995 (first entry)
XX
DE Primer for 5' end of cyclooxygenase-2.
XX
KW Cyclooxygenase-2; primer; ss; polymerase chain reaction;
KW osteosarcoma.
XX
OS Homo sapiens.
XX
PN WO9414977-A.
XX
PD 07-JUL-1994.
XX
PF 17-DEC-1993; 93WO-CA00547.
XX
PR 22-DEC-1992; 92US-0994760.
PR 06-MAY-1993; 93US-0064271.
XX
PA (MERI) MERCK FROSST CANADA INC.
XX
PI Cromlish WA, Kennedy BP, Mancini JA, O'Neill G, Vickers PJ;
PI Wong E;
XX
DR WPI; 1994-263635/32.
XX
PT Assays for cyclo:oxygenase-1 and -2 - for identifying selective
PT antagonists, i.e. potential anti inflammatories etc., also new
PT human cyclo:oxygenase-2 and cDNA encoding it

```
XX
PS   Example 43; Page 23; 55pp; English.
XX
CC   The primer corresponds to the 3' end of the cyclooxygenase-2 (COX2)
CC   cDNA sequence, and is used with Q70998 in a reverase transcription
CC   polymerase chain reaction analysis of osteosarcoma 143.98.2
CC   cells. Results with this primer pair indicate that osteosarcoma
CC   cells express COX-2 mRNA.  The COX-2 protein is used in assays to
CC   identify inhibitors which have antiinflammatory, antipyretic,
CC   analgesic and anticancer activity.
XX
SQ   Sequence 23 BP; 1 A; 11 C; 7 G; 4 T; 0 other;


  Query Match            100.0%;  Score 19;  DB 15;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 4.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db     21 GGGCGCGGGCGAGCATCGC 3


RESULT   2
Q89384/c
ID   Q89384 standard; cDNA; 23 BP.
XX
AC   Q89384;
XX
DT   28-SEP-1995  (first entry)
XX
DE   COX-2 PCR 5' primer HCOX-1.
XX
KW   Cyclooxygenase-2; COX-2; COX-1; inhibitor; screening;
KW   osteosarcoma; glyceraldehyde-3-phosphate-dehydrogenase;
KW   G3PDH; primer; PCR; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9509238-A.
XX
PD   06-APR-1995.
XX
PF   13-SEP-1994;   94WO-CA00501.
XX
PR   27-SEP-1993;   93US-0084033.
XX
PA   (MERI ) MERCK FROSST CANADA INC.
XX
PI   Mancini JA,  O'Neil GP;
XX
DR   WPI; 1995-147436/19.
XX
PT   High level expression of human cyclo:oxygenase (COX)-2  - using
PT   new 3' flanking region from COX-1, useful in assays for
PT   identifying potent, selective or preferential inhibitors of COX-2
XX
PS   Example 4; Page 24; 59pp; English.
XX
CC   The primers given in Q89384-85, corresp. to the 5' and 3' ends of
CC   COX-2 cDNA, were used in RT-PCR of human osteosarcoma 143 cell
CC   line total RNA to amplify COX-2 mRNA.
XX
SQ   Sequence 23 BP; 1 A; 11 C; 7 G; 4 T; 0 other;


  Query Match            100.0%;  Score 19;  DB 16;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 4.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db     21 GGGCGCGGGCGAGCATCGC 3


RESULT   3
C57690/c
ID   C57690 standard; DNA; 429 BP.
XX
AC   C57690;
XX
DT   25-JAN-2001  (first entry)
XX
DE   Arachidonic acid metabolism related genomic biallelic marker #324.
XX
KW   Human; biallelic marker; arachidonic acid metabolism; genotyping;
KW   detection; hybridisation; phenotype; haplotype; SNP; polymorphic base;
KW   single nucleotide polymorphism; hybridisation assay; sequencing assay;
KW   specific amplification assay; identification; ERBM; 12-LO-RBM;
KW   eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.
XX
OS   Homo sapiens.
XX
PN   WO200047771-A2.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-IB00184.
XX
PR   12-FEB-1999;   99US-0119917.
PR   23-MAR-1999;   99US-0275267.
PR   07-MAY-1999;   99US-0133200.
XX
PA   (GEST ) GENSET.
XX
PI   Blumenfeld M,  Bougueleret L,  Chumakov I;
XX
DR   WPI; 2000-571881/53.
XX
PT   Novel biallelic markers useful for detecting conditions and genotypes
PT   associated with arachidonic acid metabolism -
XX
PS   Claim 13; Page 508; 802pp; English.
XX
CC   The present invention describes polynucleotides including biallelic
CC   markers derived from genes involved in arachidonic acid metabolism and
CC   from genomic regions flanking those genes. Methods from the present
CC   invention may be used to select individuals for clinical trials and
CC   predict responses to treatment with drugs. The polynucleotides may be
CC   used in hybridisation assays, sequencing assays and specific
CC   amplification assays for identifying an eicosanoid-related biallelic
CC   marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a
CC   segment of nucleotides containing an ERBM. The polynucleotides are
CC   useful in diagnostic kits. The markers may be used to detect conditions
CC   and genotypes associated with arachidonic acid metabolism. C57367 to
CC   C58018 and B24019 and B24020 represent sequences used in the
CC   exemplification of the present invention.
CC   N.B. Polymorphic bases (single nucleotide polymorphisms also known as
CC   SNPs) in the polynucleotide sequences from the present invention have
CC   been given as their corresponding degenerate bases e.g. a polymorphic
CC   base of C or T has been given as Y.
XX
SQ   Sequence 429 BP; 84 A; 144 C; 113 G; 86 T; 2 other;


  Query Match            100.0%;  Score 19;  DB 21;  Length 429;
  Best Local Similarity  100.0%;  Pred. No. 3.7;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db    200 GGGCGCGGGCGAGCATCGC 182


RESULT   4
Q61790/c
```

```
ID   Q61790 standard; cDNA; 1834 BP.
XX
AC   Q61790;
XX
DT   12-OCT-1994  (first entry)
XX
DE   Sequence of human prostaglandin G/H synthase-2 (PGHS-2).
XX
KW   Prostaglandin; hormone; eicosanoid; fatty acid metabolism; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             9..1823
FT                   /*tag=  a
XX
PN   WO9406919-A.
XX
PD   31-MAR-1994.
XX
PF   22-SEP-1993;   93WO-US09167.
XX
PR   22-SEP-1992;   92US-0949780.
PR   01-DEC-1992;   92US-0983835.
PR   22-MAR-1993;   93US-0034143.
PR   28-APR-1993;   93US-0054364.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Obanion MK,  Winn VD,  Young DA;
XX
DR   WPI; 1994-118468/14.
DR   P-PSDB; R51267.
XX
PT   New prostaglandin G/H synthase-2 gene - used for producing
PT   transgenic cell lines for testing ability of cpds. to inhibit
PT   synthesis of prostaglandin(s)
XX
PS   Claim 38; Page 43-44; 76pp; English.
XX
CC   RNA was isolated from a human fibroblast cell line (W138). PCR
CC   primers specific for the human PGHS-1 and PGHS-2 sequences were
CC   engineered to amplify the coding regions of either one transcript or
CC   the other (see Q61792-95). PCR products of about 2 kb were generated.
CC   Three PGHS-2 clones were sequenced in both directions. The clone
CC   comprising the PGHS-2 sequence disclosed in Q61790 was selected for
CC   transfection. This sequence differs from the human PGHS-2 sequence
CC   dislcosed by Hla and Heilson, PNAS, 89, 7384 (19920 due to a Glu
CC   rather than a Gly at AA posn. 165. Mouse PGHS-2 also has a Glu at
CC   this posn.
XX
SQ   Sequence 1834 BP; 518 A; 435 C; 391 G; 490 T; 0 other;


  Query Match             100.0%;  Score 19;  DB 15;  Length 1834;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||||||||
Db     24 GGGCGCGGGCGAGCATCGC 6


RESULT   5
T59635/c
ID   T59635 standard; DNA; 1834 BP.
XX
AC   T59635;
XX
DT   04-MAY-1997  (first entry)
XX
DE   Human prostaglandin H synthase-2 gene.
XX
KW   Prostaglandin H synthase-2; PGHS-2; cyclooxygenase; inflammation;
KW   pulmonary fibrosis; Alzheimer's disease; stroke; acute head injury;
KW   endometriosis; dysmenorrhea; pre-term labour; prostate cancer;
KW   colorectal cancer; squamous cell carcinoma; breast cancer;
KW   oral pharyngeal cancer; stomach cancer; fibrosarcoma; skin cancer;
KW   osteosarcoma; antiinflammatory; antisense; ribozyme; triple helix;
KW   gene therapy; diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             9..1823
FT                   /*tag=  a
FT   misc_feature    1375..1405
FT                   /*tag=  b
FT                   /note= "bases 1375-1405 show substantial divergence
FT                          from the mouse PGHS-2 gene"
FT   misc_feature    1797..1827
FT                   /*tag=  c
FT                   /note= "bases 1797-1827 show substantial divergence
FT                          from the mouse PGHS-2 gene"
XX
PN   WO9640720-A1.
XX
PD   19-DEC-1996.
XX
PF   03-JUN-1996;   96WO-US08311.
XX
PR   07-JUN-1995;   95US-0487752.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   O'Banion MK,  Winn VD,  Young DA;
XX
DR   WPI; 1997-052220/05.
DR   P-PSDB; W12698.
XX
PT   Nucleic acid encoding human prostaglandin H synthase-2 - used in
PT   treating and detection of inflammation, pre-term labour, cancer, etc
XX
PS   Example 9; Fig 6a-b; 126pp; English.
XX
CC   A DNA clone (T59635) codes for human glucocorticoid-regulated
CC   prostaglandin H synthase 2 (PGHS-2) (W12698), an enzyme responsible
CC   for increased prostaglandin synthesis associated with inflammation.
CC   It was obtd. by PCR amplification of RNA isolated from serum- and
CC   cycloheximide-treated human fibroblast W138 cells, using PGHS-2-
CC   specific primers (see also T59638-39).  The gene can be used to
CC   express recombinant PGHS-2 in transformed host cells for use in
CC   identifying cpds. that inhibit PGHS-2.  It can also be used to
CC   detect expression of PGHS-2 as a means of diagnosing certain
CC   cancers.  Antisense, ribozyme and triple helix constructs can be
CC   used to treat e.g. inflammation, pulmonary fibrosis, Alzheimer's
CC   disease, stroke, acute head injury, endometriosis, dysmenorrhea,
CC   pre-term labour, cancer and radiation-induced injury.
XX
SQ   Sequence 1834 BP; 517 A; 431 C; 397 G; 489 T; 0 other;


  Query Match             100.0%;  Score 19;  DB 18;  Length 1834;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||||||||
Db     24 GGGCGCGGGCGAGCATCGC 6


RESULT   6
Q71002/c
ID   Q71002 standard; cDNA; 3387 BP.
XX
AC   Q71002;
```

```
XX
DT   27-FEB-1995  (first entry)
XX
DE   Cyclooxygenase-2 cDNA.
XX
KW   Cyclooxygenase-2; enzyme; osteosarcoma; assay; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             97..1910
FT                   /*tag= a
FT                   /label= cyclooxygenase-2
XX
PN   WO9414977-A.
XX
PD   07-JUL-1994.
XX
PF   17-DEC-1993;   93WO-CA00547.
XX
PR   22-DEC-1992;   92US-0994760.
PR   06-MAY-1993;   93US-0064271.
XX
PA   (MERI ) MERCK FROSST CANADA INC.
XX
PI   Cromlish WA,  Kennedy BP,  Mancini JA,  O'Neill G,  Vickers PJ;
PI    Wong E;
XX
DR   WPI; 1994-263635/32.
DR   P-PSDB; R56660.
XX
PT   Assays for cyclo:oxygenase-1 and -2 - for identifying selective
PT   antagonists, i.e. potential anti inflammatories etc., also new
PT   human cyclo:oxygenase-2 and cDNA encoding it
XX
PS   Disclosure; Fig 2A-2C; 55pp; English.
XX
CC   The human cyclooxygenase-2 cDNA is isolated from osteosarcoma
CC   cells, and is expressed from a mammalian or eukaryotic vector.  The
CC   COX-2 protein is used in assays to identify inhibitors which have
CC   antiinflammatory, antipyretic, analgesic and anticancer activity.
XX
SQ   Sequence 3387 BP; 1010 A; 715 C; 631 G; 1031 T; 0 other;


  Query Match             100.0%;  Score 19;  DB 15;  Length 3387;
  Best Local Similarity   100.0%;  Pred. No. 3.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           |||||||||||||||||||
Db     113 GGGCGCGGGCGAGCATCGC 95


RESULT   7
Q89376/c
ID   Q89376 standard; cDNA; 3387 BP.
XX
AC   Q89376;
XX
DT   28-SEP-1995  (first entry)
XX
DE   Human cyclooxygenase-2 cDNA.
XX
KW   Cyclooxygenase-2; COX-2; COX-1; inhibitor; screening;
KW   osteosarcoma; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             98..1912
FT                   /*tag= a
XX
PN   WO9509238-A.
XX
PD   06-APR-1995.
XX
PF   13-SEP-1994;   94WO-CA00501.
XX
PR   27-SEP-1993;   93US-0084033.
XX
PA   (MERI ) MERCK FROSST CANADA INC.
XX
PI   Mancini JA,  O'Neil GP;
XX
DR   WPI; 1995-147436/19.
DR   P-PSDB; R72228.
XX
PT   High level expression of human cyclo:oxygenase (COX)-2  - using
PT   new 3' flanking region from COX-1, useful in assays for
PT   identifying potent, selective or preferential inhibitors of COX-2
XX
PS   Disclosure; Fig.2; 59pp; English.
XX
CC   Full-length cDNA derived from human osteosarcoma cells (given in
CC   Q89376) encoded human COX-2 (R72228).  High-level expression of COX-2
CC   in COS7 cells was achieved using a vaccinia or baculovirus vector and
CC   a construct in which COX-2 cDNA was attached at its 5' end to a 3'
CC   flanking sequence of human COX-1 cDNA (Q89377).
XX
SQ   Sequence 3387 BP; 1010 A; 714 C; 632 G; 1031 T; 0 other;


  Query Match             100.0%;  Score 19;  DB 16;  Length 3387;
  Best Local Similarity   100.0%;  Pred. No. 3.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           |||||||||||||||||||
Db     113 GGGCGCGGGCGAGCATCGC 95


RESULT   8
F21115/c
ID   F21115 standard; DNA; 3387 BP.
XX
AC   F21115;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human low adenosine antisense oligonucleotide related sequence #2682.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
```

PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 965-966; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 3387 BP; 1010 A; 712 C; 633 G; 1032 T; 0 other;

Query Match 100.0%; Score 19; DB 21; Length 3387;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCGCGGGCGAGCATCGC 19
||||||||||||||||||||
Db 113 GGGCGCGGGCGAGCATCGC 95

RESULT 9
A34993/c
ID A34993 standard; DNA; 3387 BP.
XX
AC A34993;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2682.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX

PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 890-891; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
SQ Sequence 3387 BP; 1010 A; 712 C; 633 G; 1032 T; 0 other;

Query Match 100.0%; Score 19; DB 21; Length 3387;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCGCGGGCGAGCATCGC 19
||||||||||||||||||||
Db 113 GGGCGCGGGCGAGCATCGC 95

RESULT 10
F21117/c
ID F21117 standard; DNA; 15240 BP.
XX
AC F21117;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2684.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;

KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 968-972; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 15240 BP; 4672 A; 2944 C; 2804 G; 4820 T; 0 other;

Query Match 100.0%; Score 19; DB 21; Length 15240;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCGCGGGCGAGCATCGC 19
||||||||||||||||||||
Db 2513 GGGCGCGGGCGAGCATCGC 2495

RESULT 11

A34995/c
ID A34995 standard; DNA; 15240 BP.
XX
AC A34995;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2684.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 893-897; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
SQ Sequence 15240 BP; 4672 A; 2944 C; 2804 G; 4820 T; 0 other;

Query Match 100.0%; Score 19; DB 21; Length 15240;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||||||||
Db   2513 GGGCGCGGGCGAGCATCGC 2495


RESULT  12
T08722/c
ID   T08722 standard; DNA; 654 BP.
XX
AC   T08722;
XX
DT   19-JUL-1996  (first entry)
XX
DE   Paracoccus denitrificans thiamine pyrophosphokinase gene.
XX
KW   Thiamine diphosphate biosynthesis; TPP; adenosine 5'-triphosphate;
KW   tpk gene; ss.
XX
OS   Paracoccus denitrificans (ATCC 19367).
XX
FH   Key             Location/Qualifiers
FT   mat_peptide     1..654
FT                   /*tag=  a
XX
PN   JP08009985-A.
XX
PD   16-JAN-1996.
XX
PF   01-JUL-1994;   94JP-0150847.
XX
PR   01-JUL-1994;   94JP-0150847.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
DR   WPI; 1996-110279/12.
DR   P-PSDB; R92223.
XX
PT   Paracoccus sp. transformed with thiamine pyro:phospho:kinase gene -
PT   useful for prodn. of thiamine di:phosphate from thiamine and
PT   adenosine 5'-tri:phosphate
XX
PS   Claim 8; Page 9; 11pp; Japanese.
XX
CC   The present sequence is one of the two sequences given in the
CC   specification which each code for the same 218 amino acid sequence
CC   of Paracoccus denitrificans thiamine pyrophosphokinase. Paracoccus
CC   bacteria transformed with the coding sequence are useful for
CC   increased production of thiamine diphosphate from thiamine and
CC   adenosine 5'-triphosphate.
XX
SQ   Sequence 654 BP; 83 A; 246 C; 218 G; 107 T; 0 other;


  Query Match             91.6%;  Score 17.4;  DB 17;  Length 654;
  Best Local Similarity   94.7%;  Pred. No. 19;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||| ||||
Db    652 GGGCGCGGGCGAGCGTCGC 634


RESULT  13
T08723/c
ID   T08723 standard; DNA; 654 BP.
XX
AC   T08723;
XX
DT   19-JUL-1996  (first entry)
XX
DE   Paracoccus denitrificans thiamine pyrophosphokinase gene.
XX
KW   Thiamine diphosphate biosynthesis; TPP; adenosine 5'-triphosphate;
KW   tpk gene; silent mutation; conservative codon replacement; ss.
XX
OS   Paracoccus denitrificans (ATCC 19367).
XX
FH   Key             Location/Qualifiers
FT   mat_peptide     1..654
FT                   /*tag=  a
XX
PN   JP08009985-A.
XX
PD   16-JAN-1996.
XX
PF   01-JUL-1994;   94JP-0150847.
XX
PR   01-JUL-1994;   94JP-0150847.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
DR   WPI; 1996-110279/12.
DR   P-PSDB; R92223.
XX
PT   Paracoccus sp. transformed with thiamine pyro:phospho:kinase gene -
PT   useful for prodn. of thiamine di:phosphate from thiamine and
PT   adenosine 5'-tri:phosphate
XX
PS   Claim 9; Page 9-10; 11pp; Japanese.
XX
CC   The present sequence is one of the two sequences given in the
CC   specification which each code for the same 218 amino acid sequence
CC   of Paracoccus denitrificans thiamine pyrophosphokinase. The two
CC   sequences differ by silent substitutions in codons 2-7 which were
CC   introduced into T08723 by insertion of a synthetic linker.
CC   Paracoccus bacteria transformed with the coding sequence are
CC   useful for increased production of thiamine diphosphate from
CC   thiamine and adenosine 5'-triphosphate.
XX
SQ   Sequence 654 BP; 84 A; 246 C; 216 G; 108 T; 0 other;


  Query Match             91.6%;  Score 17.4;  DB 17;  Length 654;
  Best Local Similarity   94.7%;  Pred. No. 19;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||| ||||
Db    652 GGGCGCGGGCGAGCGTCGC 634


RESULT  14
Q91482
ID   Q91482 standard; DNA; 18 BP.
XX
AC   Q91482;
XX
DT   08-FEB-1996  (first entry)
XX
DE   Human cyclooxygenase-2 antisense oligonucleotide hCOX-2.7.
XX
KW   human; cyclooxygenase-2; COX-2; prostaglandin; thromboxane;
KW   inhibition; antisense therapy; premature labour; preeclampsia;
KW   endometriosis; rheumatoid arthritis; glomerulitis; ARDS;
KW   adult respiratory distress syndrome; ss.
XX
OS   Synthetic.
XX
PN   WO9516466-A1.
XX
PD   22-JUN-1995.
XX
PF   16-DEC-1994;   94WO-US14508.
XX
PR   17-DEC-1993;   93US-0170089.
```

```
XX
PA   (OHIS ) UNIV OHIO STATE.
XX
PI   Kniss DA;
XX
DR   WPI; 1995-231361/30.
XX
PT   Anti:sense oligo:nucleotide(s) binding cyclo:oxygenase and
PT   thromboxane A2 synthase mRNA  - used in treatment of diseases
PT   involving prostaglandin(s) and thromboxane metabolism
XX
PS   Claim 2; Page 36; 50pp; English.
XX
CC   Antisense oligonucleotides were designed based on the 5'-UTR and
CC   3'-UTR sequences of mouse and human cyclooxygenase cDNAs. The
CC   phosphorothioate derivs. ("S-oligonucleotides") of the different
CC   antisense sequences were found to be effective for inhibiting
CC   translation of cyclooxygenase and subsequent production of
CC   prostaglandins and thromboxanes. The S-oligonucleotide derivs of Q91475-
CC   Q91484 are based on the human cyclooxygenase-2 cDNA and are useful
CC   for antisense therapy of ARDS, glomerulitis, rheumatoid arthritis,
CC   premature labour, preeclampsia, endometriosis, etc.
XX
SQ   Sequence 18 BP; 3 A; 5 C; 9 G; 1 T; 0 other;


  Query Match             89.5%;  Score 17;  DB 16;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATC 17
          |||||||||||||||||
Db      2 gggcgcgggcgagcatc 18


RESULT  15
F21116/c
ID   F21116 standard; DNA; 9453 BP.
XX
AC   F21116;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human low adenosine antisense oligonucleotide related sequence #2683.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Disclosure; Page 966-968; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC   and antisense oligonucleotides used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 9453 BP; 2937 A; 1716 C; 1710 G; 3090 T; 0 other;


  Query Match             89.5%;  Score 17;  DB 21;  Length 9453;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATC 17
          |||||||||||||||||
Db    981 GGGCGCGGGCGAGCATC 965


Search completed: April 20, 2001, 00:12:58
Job time: 10020 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:24:55 ; Search time 7150.85 Seconds
(without alignments)
0.388 Million cell updates/sec

Title: US-09-016-464-17
Perfect score: 19
Sequence: 1 GGGCGCGGGCGAGCATCGC 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	19	100.0	1040	139	BE785396	BE785396 601478114
c	2	17.4	91.6	792	136	BE531093	BE531093 601278455
	3	17	89.5	435	232	FR0036546	AL124055 Fugu rubr
c	4	16.4	86.3	346	213	AQ910758	AQ910758 GSSTc0359
	5	16.4	86.3	595	165	BE336923	BE336923 bb68h08.y
	6	16.4	86.3	765	141	BE898809	BE898809 601681792
c	7	16.4	86.3	803	104	AJ006537	AJ006537 AJ006537
	8	16.4	86.3	805	146	BF259017	BF259017 HVSMEf001
c	9	16.4	86.3	865	212	AQ858748	AQ858748 nbeb0002D
c	10	16.4	86.3	912	212	AQ872091	AQ872091 nbeb0046H
c	11	16	84.2	605	232	FR0036531	AL124040 Fugu rubr
	12	16	84.2	1582	145	BF255067	BF255067 HVSMEf000
c	13	15.8	83.2	239	31	AV640162	AV640162 AV640162
c	14	15.8	83.2	264	161	BB595164	BB595164 BB595164
c	15	15.8	83.2	334	116	AW487153	AW487153 81177 MAR
c	16	15.8	83.2	348	137	BE587114	BE587114 WHE0517_E
	17	15.8	83.2	352	9	AA587234	AA587234 nn82c10.s
c	18	15.8	83.2	369	20	AI414040	AI414040 ma03g10.x

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c	20	15.8	83.2	379	167	BE484722	BE484722 171474 BA
c	21	15.8	83.2	382	116	AW487170	AW487170 81223 MAR
c	22	15.8	83.2	399	116	AW489298	AW489298 UI-M-BH3-
	23	15.8	83.2	400	227	B07847	B07847 GR0518T32 R
c	24	15.8	83.2	434	115	AW447389	AW447389.88908 MAR
c	25	15.8	83.2	444	115	AW456157	AW456157 UI-M-BH3-
c	26	15.8	83.2	464	143	BF039865	BF039865 BP250025A
	27	15.8	83.2	473	137	BE604159	BE604159 WHE1413-1
c	28	15.8	83.2	491	167	BE487654	BE487654 176714 BA
c	29	15.8	83.2	509	30	AV594128	AV594128 AV594128
c	30	15.8	83.2	526	30	AV592535	AV592535 AV592535
c	31	15.8	83.2	534	167	BE484579	BE484579 171283 BA
c	32	15.8	83.2	537	31	AV666430	AV666430 AV666430
c	33	15.8	83.2	544	30	AV597886	AV597886 AV597886
c	34	15.8	83.2	544	31	AV663454	AV663454 AV663454
c	35	15.8	83.2	545	137	BE588589	BE588589 193785 BA
c	36	15.8	83.2	549	148	BF466887	BF466887 UI-M-CG0p
c	37	15.8	83.2	556	30	AV597960	AV597960 AV597960
c	38	15.8	83.2	559	30	AV599540	AV599540 AV599540
c	39	15.8	83.2	562	30	AV607714	AV607714 AV607714
c	40	15.8	83.2	574	30	AV592392	AV592392 AV592392
c	41	15.8	83.2	582	30	AV594173	AV594173 AV594173
c	42	15.8	83.2	588	14	AB009110	AB009110 AB009110
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c	44	15.8	83.2	596	30	AV595105	AV595105 AV595105
c	45	15.8	83.2	610	30	AV596710	AV596710 AV596710

ALIGNMENTS

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RESULT   1
BE785396/c
LOCUS       BE785396      1040 bp    mRNA            EST       20-OCT-2000
DEFINITION  601478114F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880850 5',
            mRNA sequence.
ACCESSION   BE785396
VERSION     BE785396.1  GI:10206594
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1040)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9648  row: l  column: 03
            High quality sequence stop: 649.
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                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
BASE COUNT      307 a    314 c    231 g    188 t
ORIGIN


  Query Match             100.0%;  Score 19;  DB 139;  Length 1040;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db    118 GGGCGCGGGCGAGCATCGC 100


RESULT   2
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LOCUS       BE531093      792 bp    mRNA            EST       09-AUG-2000
DEFINITION  601278455F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610573 5',
            mRNA sequence.
ACCESSION   BE531093
VERSION     BE531093.1  GI:9759738
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 792)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM266  row: n  column: 14
            High quality sequence stop: 606.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3610573"
                     /clone_lib="NIH_MGC_39"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Library constructed
                     by Ling Hong in the laboratory of Gerald M. Rubin
                     (University of California,  Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies)."
BASE COUNT      105 a    290 c    284 g    113 t
ORIGIN


  Query Match             91.6%;  Score 17.4;  DB 136;  Length 792;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||| ||||||||
Db    599 GGGCGCGGGCCAGCATCGC 581


RESULT   3
FR0036546
LOCUS       FR0036546     435 bp    DNA             GSS       22-OCT-1999
DEFINITION  Fugu rubripes GSS sequence, clone 032A03aC3, genomic survey
```

```
            sequence.
ACCESSION   AL124055
VERSION     AL124055.1  GI:6105670
KEYWORDS    GSS; genome survey sequence.
SOURCE      Fugu rubripes.
  ORGANISM  Fugu rubripes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
            Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
REFERENCE   1  (bases 1 to 435)
  AUTHORS   Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,
            Umrania,Y., Williams,G. and Brenner,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
            Centre, Hinxton, Cambridge, CB10 1SB. UK Email:
            biohelp@hgmp.mrc.ac.uk
COMMENT     Vector: pBluescript II KS
            V_type: phagemid
            PRIMER: KS
            DESCR:
            One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.
FEATURES             Location/Qualifiers
     source          1. .435
                     /organism="Fugu rubripes"
                     /db_xref="taxon:31033"
                     /clone_lib="cosmid 032A03"
                     /clone="032A03aC3"
BASE COUNT      109 a    104 c     95 g     99 t     28 others
ORIGIN


  Query Match             89.5%;  Score 17;  DB 232;  Length 435;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATC 17
           |||||||||||||||||
Db      57 GGGCGCGGGCGAGCATC 73


RESULT   4
AQ910758/c
LOCUS       AQ910758      346 bp    DNA             GSS       09-JAN-2001
DEFINITION  GSSTc03594 Trypanosoma cruzi random genomic library Trypanosoma
            cruzi genomic clone G45E4, DNA sequence.
ACCESSION   AQ910758
VERSION     AQ910758.3  GI:10137442
KEYWORDS    GSS.
SOURCE      Trypanosoma cruzi.
  ORGANISM  Trypanosoma cruzi
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma; Schizotrypanum.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
  TITLE     A random sequencing approach for the analysis of the trypanosoma
            cruzi genome: general structure, large gene and repetitive DNA
            families, and gene discovery
  JOURNAL   Genome Res. 10 (12), 1996-2005 (2000)
  MEDLINE   20568489
COMMENT     On Sep 14, 2000 this sequence version replaced gi:9378219.
            Contact: Sanchez D.O.
            Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
            San Martin)
            Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24
            CP(1650) San Martin, Prov. de BS AS. Argentina
            Tel: 54-11-4580-7255 ext 309
            Fax: 54-11-4752-9639
            Email: dsanchez@iib.unsam.edu.ar
            Sequences were basecalled with phred and vector was masked with
            crossmatch (see http://genome.washington.edu). Sequences were then
            trimmed from both ends to remove low quality bases and masked
            vector.
            Seq primer: T7
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Trypanosoma cruzi"
                     /strain="CL-Brener"
                     /db_xref="taxon:5693"
                     /clone="G45E4"
                     /clone_lib="Trypanosoma cruzi random genomic library"
                     /cell_type="epimastigote"
                     /note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
                     randomly sheared using a nebulizer and the 1 to 2 Kb range
                     was gel purified and cloned into the dephosphoryated
                     HincII site of the vector"
BASE COUNT       81 a     89 c    105 g     71 t
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 213;  Length 346;
  Best Local Similarity   94.4%;  Pred. No. 5.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCG 18
           |||||| ||||||||||
Db     310 GGGCGCTGGCGAGCATCG 293


RESULT   5
BE336923
LOCUS       BE336923      595 bp    mRNA            EST       14-JUL-2000
DEFINITION  bb68h08.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030687 5'
            similar to TR:Q24292 Q24292 ADHERIN. ;, mRNA sequence.
ACCESSION   BE336923
VERSION     BE336923.1  GI:9189308
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: bb68h08.x1
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml
            Seq primer: -40RP from Gibco
            High quality sequence stop: 501.
FEATURES             Location/Qualifiers
     source          1. .595
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3030687"
                     /clone_lib="NIH_MGC_9"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      130 a    197 c    169 g     99 t
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ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 165;  Length 595;
  Best Local Similarity   94.4%;  Pred. No. 5.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCG 18
          |||||||||||||||| ||
Db    368 GGGCGCGGGCGAGCAGCG 385


RESULT   6
BE898809
LOCUS       BE898809      765 bp    mRNA            EST       29-SEP-2000
DEFINITION  601681792F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951814 5',
            mRNA sequence.
ACCESSION   BE898809
VERSION     BE898809.1  GI:10365660
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 765)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM820  row: h  column: 23
            High quality sequence stop: 754.
FEATURES             Location/Qualifiers
     source          1. .765
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3951814"
                     /clone_lib="NIH_MGC_9"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      169 a    236 c    210 g    150 t
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 141;  Length 765;
  Best Local Similarity   94.4%;  Pred. No. 5.1e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCG 18
          |||||||||||||||| ||
Db    350 GGGCGCGGGCGAGCAGCG 367


RESULT   7
AJ006537/c
LOCUS       AJ006537      803 bp    mRNA            EST       02-JUN-1998
DEFINITION  AJ006537 Zea mays early female inflorescence Zea mays cDNA clone
            gcM2, mRNA sequence.
ACCESSION   AJ006537
VERSION     AJ006537.1  GI:3172006
KEYWORDS    EST.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
            ; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 803)
  AUTHORS   Cardon,G.H. and Huijser,P.
  TITLE     Zea mays mRNA (Cardon,G.H. and Huijser,P.)
  JOURNAL   Unpublished (1998)
COMMENT     Contact: G.H. Cardon
            Molecular Plant Genetics
            Max-Planck-Institut fuer Zuechtungsforschung
            Carl-von-Linne-Weg 10, 50829, Germany
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .803
                     /organism="Zea mays"
                     /cultivar="T232"
                     /db_xref="taxon:4577"
                     /clone="gcM2"
                     /clone_lib="Zea mays early female inflorescence"
                     /sex="female"
                     /tissue_type="early inflorescence"
                     /note="Vector: lambda-ZAP"
BASE COUNT      127 a    239 c    274 g    162 t      1 others
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 104;  Length 803;
  Best Local Similarity   94.4%;  Pred. No. 5.1e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 GGCGCGGGCGAGCATCGC 19
          ||||| ||||||||||||
Db    365 GGCGCTGGCGAGCATCGC 348


RESULT   8
BF259017
LOCUS       BF259017      805 bp    mRNA            EST       16-NOV-2000
DEFINITION  HVSMEf0017G12f Hordeum vulgare seedling root EST library HVcDNA0007
            (etiolated and unstressed) Hordeum vulgare cDNA clone
            HVSMEf0017G12f, mRNA sequence.
ACCESSION   BF259017
VERSION     BF259017.1  GI:11188130
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
            Hordeum.
REFERENCE   1  (bases 1 to 805)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
            ,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
            Wood,T.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence start: 2
            High quality sequence stop: 707.
FEATURES             Location/Qualifiers
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     source          1. .805
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEf0017G12f"
                     /clone_lib="Hordeum vulgare seedling root EST library
                     HVcDNA0007 (etiolated and unstressed)"
                     /tissue_type="Seedling root"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1"
BASE COUNT      202 a    212 c    195 g    196 t
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 146;  Length 805;
  Best Local Similarity   94.4%;  Pred. No. 5.1e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 GGCGCGGGCGAGCATCGC 19
           |||||||||| |||||||
Db     266 GGCGCGGGCGCGCATCGC 283


RESULT   9
AQ858748/c
LOCUS       AQ858748      865 bp    DNA             GSS       03-NOV-1999
DEFINITION  nbeb0002D04r CUGI Rice BAC Library (EcoRI) Oryza sativa genomic
            clone nbeb0002D04r, DNA sequence.
ACCESSION   AQ858748
VERSION     AQ858748.1  GI:6209205
KEYWORDS    GSS.
SOURCE      Oryza sativa.
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
            Oryza.
REFERENCE   1  (bases 1 to 865)
  AUTHORS   Wing,R.A. and Dean,R.A.
  TITLE     A BAC End Sequencing Framework to Sequence the Rice Genome
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: GGAAACAGCTATGACCATG
            Class: BAC ends
            High quality sequence start: 19
            High quality sequence stop: 501.
FEATURES             Location/Qualifiers
     source          1. .865
                     /organism="Oryza sativa"
                     /strain="Japonica"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:4530"
                     /clone="nbeb0002D04r"
                     /clone_lib="CUGI Rice BAC Library (EcoRI)"
                     /tissue_type="Leaf"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI;
                     Rice is the most important food crop in the world. Half of
                     the world population, especially those inhabiting highly
                     populated areas of the humid tropics and subtropics, rely
                     on rice as their primary source of carbohydrate.
                     Monocotyledonous rice is a diploid plant (2n=24) with a
                     haploid genome equivalent of 431 Mbp (Arumuganathan and
                     Earle, 1991). The relatively small genome of rice, three
                     times larger than that of Arabidopsis, makes it suitable
                     for genomic studies. In order to facilitate positional
                     cloning, physical mapping and genome sequencing of rice,
                     we have constructed a BAC library from Oryza sativa,
                     Nipponbare variety using EcoRI as the cloning enzyme. The
                     library contains 55,296 clones with an average insert size
                     of 121 Kb providing approximatley 15 haploid genome
                     equivalents. The deep coverage allows the isolation a
                     particular sequence with a probability of 99.9 %. Three
                     high density filters, each containing 18,432 clones
                     (doubly spotted), represent the whole library for colony
                     screening and can be requested from the Clemson University
                     BAC/EST Resource Center (www.genome.clemson.edu)."
BASE COUNT      145 a    250 c    215 g    250 t      5 others
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 212;  Length 865;
  Best Local Similarity   94.4%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 GGCGCGGGCGAGCATCGC 19
           |||||||||||||| |||
Db     695 GGCGCGGGCGAGCACCGC 678


RESULT  10
AQ872091/c
LOCUS       AQ872091      912 bp    DNA             GSS       03-NOV-1999
DEFINITION  nbeb0046H11f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic
            clone nbeb0046H11f, DNA sequence.
ACCESSION   AQ872091
VERSION     AQ872091.1  GI:6222542
KEYWORDS    GSS.
SOURCE      Oryza sativa.
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
            Oryza.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   Wing,R.A. and Dean,R.A.
  TITLE     A BAC End Sequencing Framework to Sequence the Rice Genome
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            Class: BAC ends
            High quality sequence start: 174
            High quality sequence stop: 310.
FEATURES             Location/Qualifiers
     source          1. .912
                     /organism="Oryza sativa"
                     /strain="Japonica"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:4530"
                     /clone="nbeb0046H11f"
                     /clone_lib="CUGI Rice BAC Library (EcoRI)"
                     /tissue_type="Leaf"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI;
                     Rice is the most important food crop in the world. Half of
                     the world population, especially those inhabiting highly
                     populated areas of the humid tropics and subtropics, rely
                     on rice as their primary source of carbohydrate.
                     Monocotyledonous rice is a diploid plant (2n=24) with a
                     haploid genome equivalent of 431 Mbp (Arumuganathan and
                     Earle, 1991). The relatively small genome of rice, three
                     times larger than that of Arabidopsis, makes it suitable
                     for genomic studies. In order to facilitate positional
                     cloning, physical mapping and genome sequencing of rice,
                     we have constructed a BAC library from Oryza sativa,
                     Nipponbare variety using EcoRI as the cloning enzyme. The
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                library contains 55,296 clones with an average insert size
                of 121 Kb providing approximatley 15 haploid genome
                equivalents. The deep coverage allows the isolation a
                particular sequence with a probability of 99.9 %. Three
                high density filters, each containing 18,432 clones
                (doubly spotted), represent the whole library for colony
                screening and can be requested from the Clemson University
                BAC/EST Resource Center (www.genome.clemson.edu)."
BASE COUNT      235 a    269 c    245 g    160 t      3 others
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 212;  Length 912;
  Best Local Similarity   94.4%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCG 18
          |||||||||||| ||||||
Db    123 GGGCGCGGGCGCGCATCG 106


RESULT  11
FR0036531/c
LOCUS       FR0036531     605 bp    DNA             GSS       22-OCT-1999
DEFINITION  Fugu rubripes GSS sequence, clone 032A03aH9, genomic survey
            sequence.
ACCESSION   AL124040
VERSION     AL124040.1  GI:6105655
KEYWORDS    GSS; genome survey sequence.
SOURCE      Fugu rubripes.
  ORGANISM  Fugu rubripes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
            Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
REFERENCE   1  (bases 1 to 605)
  AUTHORS   Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,
            Umrania,Y., Williams,G. and Brenner,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
            Centre, Hinxton, Cambridge, CB10 1SB. UK Email:
            biohelp@hgmp.mrc.ac.uk
COMMENT     Vector: pBluescript II KS
            V_type: phagemid
            PRIMER: KS
            DESCR:
            One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.
FEATURES             Location/Qualifiers
     source          1. .605
                     /organism="Fugu rubripes"
                     /db_xref="taxon:31033"
                     /clone_lib="cosmid 032A03"
                     /clone="032A03aH9"
BASE COUNT      162 a    138 c    135 g    150 t     20 others
ORIGIN


  Query Match             84.2%;  Score 16;  DB 232;  Length 605;
  Best Local Similarity   94.1%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATC 17
          ||| ||||||||||||
Db    144 GGGNGCGGGCGAGCATC 128


RESULT  12
BF255067
LOCUS       BF255067     1582 bp    mRNA            EST       16-NOV-2000
DEFINITION  HVSMEf0005N17f Hordeum vulgare seedling root EST library HVcDNA0007
            (etiolated and unstressed) Hordeum vulgare cDNA clone
            HVSMEf0005N17f, mRNA sequence.
ACCESSION   BF255067
VERSION     BF255067.1  GI:11184172
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
            Hordeum.
REFERENCE   1  (bases 1 to 1582)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
            ,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
            Wood,T.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence start: 414
            High quality sequence stop: 1089.
FEATURES             Location/Qualifiers
     source          1. .1582
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEf0005N17f"
                     /clone_lib="Hordeum vulgare seedling root EST library
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                     /tissue_type="Seedling root"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1"
BASE COUNT      340 a    115 c    622 g    490 t     15 others
ORIGIN


  Query Match             84.2%;  Score 16;  DB 145;  Length 1582;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCAT 16
          ||||||||||||||||
Db   1234 GGGCGCGGGCGAGCAT 1249


RESULT  13
AV640162/c
LOCUS       AV640162      239 bp    mRNA            EST       15-DEC-2000
DEFINITION  AV640162 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
            cDNA clone HCL011e01_r 5', mRNA sequence.
ACCESSION   AV640162
VERSION     AV640162.1  GI:10783490
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii.
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 239)
  AUTHORS   Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
            Nakamura,Y. and Tabata,S.
  TITLE     Generation of expressed sequence tags from low-CO2 and high-CO2
            adapted cells of Chlamydomonas reinhardtii
  JOURNAL   DNA Res. 7 (5), 305-307 (2000)
  MEDLINE   20539644
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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FEATURES             Location/Qualifiers
     source          1. .239
                     /organism="Chlamydomonas reinhardtii"
                     /strain="C9"
                     /db_xref="taxon:3055"
                     /clone="HCL011e01_r"
                     /clone_lib="Chlamydomonas reinhardtii 5% CO2"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from cells cultured
                     in a medium with bubbling air containing 5% carbon
                     dioxide"
BASE COUNT       51 a     99 c     38 g     51 t
ORIGIN


  Query Match             83.2%;  Score 15.8;  DB 31;  Length 239;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
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Db     101 GGGCGCTGGCGAGCATGGC 83


RESULT  14
BB595164/c
LOCUS       BB595164      264 bp    mRNA            EST       30-NOV-2000
DEFINITION  BB595164 RIKEN full-length enriched, adult male corpus striatum Mus
            musculus cDNA clone C030004N01 5', mRNA sequence.
ACCESSION   BB595164
VERSION     BB595164.1  GI:11491766
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 264)
  AUTHORS   Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P.
            , Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y.,
            Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno
            ,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K.,
            Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C.,
            Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A.,
            Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka
            ,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome-res@rtc.riken.go.jp,
            URL:http://genome.rtc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
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FEATURES             Location/Qualifiers
     source          1. .264
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="C030004N01"
                     /clone_lib="RIKEN full-length enriched, adult male corpus
                     striatum"
                     /sex="male"
                     /tissue_type="corpus striatum"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 185.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI"
BASE COUNT       42 a     94 c     79 g     49 t
ORIGIN


  Query Match             83.2%;  Score 15.8;  DB 161;  Length 264;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
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Db     186 GGGCGCGGGAGAGCAGCGC 168


RESULT  15
AW487153/c
LOCUS       AW487153      334 bp    mRNA            EST       10-JUL-2000
DEFINITION  81177 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   AW487153
VERSION     AW487153.1  GI:7057259
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
            Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
            ,W.W. and Keele,J.W.
  TITLE     Design and use of four pooled tissue normalized cDNA libraries for
            EST discovery in cattle
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
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            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 44  row: F  column: 10
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .334
                      /organism="Bos taurus"
                      /db_xref="taxon:9913"
                      /clone_lib="MARC 1BOV"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                      Library made from pooled tissue from lymph node, ovary,
                      fat, hypothalamus, and pituitary."
BASE COUNT       82 a     89 c    101 g     62 t
ORIGIN


  Query Match             83.2%;  Score 15.8;  DB 116;  Length 334;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           |||||||||| | ||||||
Db     283 GGGCGCGGGCCACCATCGC 265


Search completed: April 19, 2001, 23:24:57
Job time: 8174 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:03:43 ; Search time 280.46 Seconds
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11.829 Million cell updates/sec

Title: US-09-016-464-17
Perfect score: 19
Sequence: 1 GGGCGCGGGCGAGCATCGC 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	19	100.0	23	1	US-08-064-271-8	Sequence 8, Appli
c 2	19	100.0	23	4	US-08-930-589A-8	Sequence 8, Appli
c 3	19	100.0	1834	1	US-08-487-753-3	Sequence 3, Appli
c 4	19	100.0	1834	1	US-08-487-753-14	Sequence 14, Appl
c 5	19	100.0	1834	2	US-08-480-065-3	Sequence 3, Appli
c 6	19	100.0	1834	2	US-08-480-065-14	Sequence 14, Appl
c 7	19	100.0	1834	3	US-08-487-744-3	Sequence 3, Appli
c 8	19	100.0	1834	3	US-08-487-744-14	Sequence 14, Appl
c 9	19	100.0	1834	5	PCT-US93-09167-3	Sequence 3, Appli
c 10	19	100.0	3387	1	US-08-064-271-11	Sequence 11, Appl
c 11	19	100.0	3387	2	US-08-627-254C-29	Sequence 29, Appl
12	17	89.5	18	2	US-08-627-254C-16	Sequence 16, Appl
c 13	17	89.5	3387	4	US-08-930-589A-19	Sequence 19, Appl
c 14	16	84.2	41	4	US-08-930-589A-14	Sequence 14, Appl
c 15	15.8	83.2	2472	1	US-08-221-750A-2	Sequence 2, Appli
c 16	15.8	83.2	7742	1	US-08-221-750A-1	Sequence 1, Appli
17	15	78.9	15	2	US-08-627-254C-15	Sequence 15, Appl
18	15	78.9	1312	1	US-08-205-506A-1	Sequence 1, Appli
19	15	78.9	1312	5	PCT-US94-02389-1	Sequence 1, Appli
c 20	14.8	77.9	1912	2	US-08-948-569A-11	Sequence 11, Appl
c 21	14.8	77.9	1912	2	US-09-188-469-11	Sequence 11, Appl
c 22	14.8	77.9	2312	1	US-07-736-178C-1	Sequence 1, Appli
23	14.8	77.9	80161	4	US-09-036-987A-1	Sequence 1, Appli
c 24	14.2	74.7	756	1	US-07-717-332D-1	Sequence 1, Appli
c 25	14.2	74.7	1635	5	PCT-US94-05795-1	Sequence 1, Appli
26	14.2	74.7	5970	4	US-09-320-878-21	Sequence 21, Appl
c 27	14.2	74.7	6000	1	US-08-348-006B-6	Sequence 6, Appli
c 28	14.2	74.7	6000	2	US-08-800-825A-6	Sequence 6, Appli
c 29	14.2	74.7	6000	5	PCT-US94-10166-6	Sequence 6, Appli
c 30	14.2	74.7	6250	1	US-08-729-214-23	Sequence 23, Appl
c 31	14.2	74.7	6250	4	US-09-028-934-23	Sequence 23, Appl
c 32	14.2	74.7	8931	4	US-09-028-934-28	Sequence 28, Appl
33	14.2	74.7	28804	2	US-08-592-874-1	Sequence 1, Appli
34	14.2	74.7	28804	3	US-09-096-942-2	Sequence 2, Appli
35	14.2	74.7	28804	3	US-09-096-867-2	Sequence 2, Appli
c 36	14.2	74.7	28958	1	US-08-258-261B-6	Sequence 6, Appli
c 37	14.2	74.7	28958	1	US-08-456-837-6	Sequence 6, Appli
c 38	14.2	74.7	28958	1	US-08-457-342-6	Sequence 6, Appli
c 39	14.2	74.7	28958	1	US-08-457-646A-6	Sequence 6, Appli
c 40	14.2	74.7	28958	1	US-08-458-076A-6	Sequence 6, Appli
c 41	14.2	74.7	28958	1	US-08-764-233A-4	Sequence 4, Appli
c 42	14.2	74.7	28958	1	US-08-457-335A-6	Sequence 6, Appli
c 43	14.2	74.7	28958	1	US-08-729-214-6	Sequence 6, Appli
c 44	14.2	74.7	28958	4	US-09-028-934-6	Sequence 6, Appli
c 45	14.2	74.7	38506	4	US-09-320-878-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-064-271-8/c
; Sequence 8, Application US/08064271
; Patent No. 5543297
; GENERAL INFORMATION:
; APPLICANT: Kennedy, Brian P.
; APPLICANT: Cromlish, Wanda A.
; APPLICANT: Mancini, Joseph A.
; APPLICANT: O'Neil, Gary
; APPLICANT: Vickers, Philip J.
; APPLICANT: Wong, Elizabeth
; TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-2 cDNA AND
; TITLE OF INVENTION: ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in, 1.4kb
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7
; SOFTWARE: Microsoft Word 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064,271
; FILING DATE: 19930506
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Panzer, Curtis C.
; REGISTRATION NUMBER: 33,752
; REFERENCE/DOCKET NUMBER: 18906IA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3199
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-064-271-8

Query Match 100.0%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     21 GGGCGCGGGCGAGCATCGC 3


RESULT   2
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; Sequence 8, Application US/08930589A
; Patent No. 6107087
;  GENERAL INFORMATION:
;    APPLICANT:  MERCK FROSST CANADA & CO.
;    APPLICANT:  O'NEILL, GARY P.
;    APPLICANT:  MANCINI, JOSEPH A.
;    TITLE OF INVENTION:  HIGH LEVEL EXPRESSION OF HUMAN
;    TITLE OF INVENTION:  CYCLOOXYGENASE-2
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merck & Co., Inc.
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/930,589A
;      FILING DATE:  28-JUN-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coppola, Joseph A
;      REGISTRATION NUMBER:  38,413
;      REFERENCE/DOCKET NUMBER:  19029PC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  732-594-6734
;      TELEFAX:  732-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-930-589A-8


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  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
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Db     21 GGGCGCGGGCGAGCATCGC 3


RESULT   3
US-08-487-753-3/c
; Sequence 3, Application US/08487753
; Patent No. 5807733
;  GENERAL INFORMATION:
;    APPLICANT:  Young, Donald A.
;    APPLICANT:  O'Banion, Michael K.
;    APPLICANT:  Winn, Virginia D.
;    TITLE OF INVENTION:  MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
;    TITLE OF INVENTION:  FUSION PROTEINS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,753
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  3996-011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1834 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-487-753-3


  Query Match             100.0%;  Score 19;  DB 1;  Length 1834;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||||||||
Db     24 GGGCGCGGGCGAGCATCGC 6


RESULT   4
US-08-487-753-14/c
; Sequence 14, Application US/08487753
; Patent No. 5807733
;  GENERAL INFORMATION:
;    APPLICANT:  Young, Donald A.
;    APPLICANT:  O'Banion, Michael K.
;    APPLICANT:  Winn, Virginia D.
;    TITLE OF INVENTION:  MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
;    TITLE OF INVENTION:  FUSION PROTEINS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,753
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
```

```
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  3996-011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1834 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-487-753-14


  Query Match           100.0%;  Score 19;  DB 1;  Length 1834;
  Best Local Similarity  100.0%;  Pred. No. 1.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db     24 GGGCGCGGGCGAGCATCGC 6


RESULT   5
US-08-480-065-3/c
; Sequence 3, Application US/08480065
; Patent No. 5837479
;  GENERAL INFORMATION:
;    APPLICANT:  Young, Donald A.
;    APPLICANT:  O'Banion, Michael K.
;    APPLICANT:  Winn, Virginia D.
;    TITLE OF INVENTION:  SCREENIN ASSAYS FOR INHIBITORS OF
;    TITLE OF INVENTION:  MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,065
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  3996-012
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1834 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-480-065-3


  Query Match           100.0%;  Score 19;  DB 2;  Length 1834;
  Best Local Similarity  100.0%;  Pred. No. 1.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db     24 GGGCGCGGGCGAGCATCGC 6


RESULT   6
US-08-480-065-14/c
; Sequence 14, Application US/08480065
; Patent No. 5837479
;  GENERAL INFORMATION:
;    APPLICANT:  Young, Donald A.
;    APPLICANT:  O'Banion, Michael K.
;    APPLICANT:  Winn, Virginia D.
;    TITLE OF INVENTION:  SCREENIN ASSAYS FOR INHIBITORS OF
;    TITLE OF INVENTION:  MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,065
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  3996-012
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1834 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-480-065-14


  Query Match           100.0%;  Score 19;  DB 2;  Length 1834;
  Best Local Similarity  100.0%;  Pred. No. 1.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db     24 GGGCGCGGGCGAGCATCGC 6


RESULT   7
US-08-487-744-3/c
; Sequence 3, Application US/08487744
; Patent No. 6048850
;  GENERAL INFORMATION:
;    APPLICANT:  Young, Donald A.
;    APPLICANT:  O'Banion, Michael K.
;    APPLICANT:  Winn, Virginia D.
;    TITLE OF INVENTION:  METHODS FOR INHIBITING PROSTAGLANDIN
;    TITLE OF INVENTION:  SYNTHESIS IN A MAMMALIAN HOST
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
```

```
;       STREET:  1155 Avenue of the Americas
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10036-2711
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/487,744
;       FILING DATE:
;       CLASSIFICATION:  530
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Coruzzi, Laura A.
;       REGISTRATION NUMBER:  30,742
;       REFERENCE/DOCKET NUMBER:  3996-013
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1834 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  DNA (genomic)
US-08-487-744-3


  Query Match             100.0%;  Score 19;  DB 3;  Length 1834;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           |||||||||||||||||||
Db      24 GGGCGCGGGCGAGCATCGC 6


RESULT   8
US-08-487-744-14/c
; Sequence 14, Application US/08487744
; Patent No. 6048850
;  GENERAL INFORMATION:
;    APPLICANT:  Young, Donald A.
;    APPLICANT:  O'Banion, Michael K.
;    APPLICANT:  Winn, Virginia D.
;    TITLE OF INVENTION:  METHODS FOR INHIBITING PROSTAGLANDIN
;    TITLE OF INVENTION:  SYNTHESIS IN A MAMMALIAN HOST
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,744
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  3996-013
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1834 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-487-744-14


  Query Match             100.0%;  Score 19;  DB 3;  Length 1834;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           |||||||||||||||||||
Db      24 GGGCGCGGGCGAGCATCGC 6


RESULT   9
PCT-US93-09167-3/c
; Sequence 3, Application PC/TUS9309167
;  GENERAL INFORMATION:
;    APPLICANT:  Young, Donald A.
;    APPLICANT:  O'Banion, M. Kerry
;    APPLICANT:  Winn, Virginia D.
;    TITLE OF INVENTION:  Stably-Transformed Mammalian Cells
;    TITLE OF INVENTION:  Expressing a Regulated, Inflammatory Cyclooxygenase
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  3100 Norwest Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/09167
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Woessner, Warren D.
;      REGISTRATION NUMBER:  30,440
;      REFERENCE/DOCKET NUMBER:  8840.20-US-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1834 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Human PGHS-2
PCT-US93-09167-3


  Query Match             100.0%;  Score 19;  DB 5;  Length 1834;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           |||||||||||||||||||
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```
Db      24 GGGCGCGGGCGAGCATCGC 6


RESULT  10
US-08-064-271-11/c
; Sequence 11, Application US/08064271
; Patent No. 5543297
;  GENERAL INFORMATION:
;    APPLICANT:  Kennedy, Brian P.
;    APPLICANT:  Cromlish, Wanda A.
;    APPLICANT:  Mancini, Joseph A.
;    APPLICANT:  O'Neil, Gary
;    APPLICANT:  Vickers, Philip J.
;    APPLICANT:  Wong, Elizabeth
;    TITLE OF INVENTION:  HUMAN CYCLOOXYGENASE-2 cDNA AND
;    TITLE OF INVENTION:  ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merck & Co., Inc.
;      STREET:  126 Lincoln Avenue
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 in, 1.4kb
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  System 7
;      SOFTWARE:  Microsoft Word 5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/064,271
;      FILING DATE:  19930506
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Panzer, Curtis C.
;      REGISTRATION NUMBER:  33,752
;      REFERENCE/DOCKET NUMBER:  18906IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-3199
;      TELEFAX:  (908)594-4720
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3387 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-064-271-11


  Query Match             100.0%;  Score 19;  DB 1;  Length 3387;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           ||||||||||||||||||||
Db     113 GGGCGCGGGCGAGCATCGC 95


RESULT  11
US-08-627-254C-29/c
; Sequence 29, Application US/08627254C
; Patent No. 5859229
;  GENERAL INFORMATION:
;    APPLICANT:  Kniss, Douglas A.
;    TITLE OF INVENTION:  Eicosanoid Formation
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Calfee, Halter & Griwold LLP
;      STREET:  800 Superior Avenue
;      CITY:  Cleveland
;      STATE:  Ohio
;      COUNTRY:  USA
;      ZIP:  44114
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/627,254C
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Golrick, Mary E
;      REGISTRATION NUMBER:  34,829
;      REFERENCE/DOCKET NUMBER:  18525/00107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (216) 622-8200
;      TELEFAX:  (216) 241-0816
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3387 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-627-254C-29


  Query Match             100.0%;  Score 19;  DB 2;  Length 3387;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           ||||||||||||||||||||
Db     113 GGGCGCGGGCGAGCATCGC 95


RESULT  12
US-08-627-254C-16
; Sequence 16, Application US/08627254C
; Patent No. 5859229
;  GENERAL INFORMATION:
;    APPLICANT:  Kniss, Douglas A.
;    TITLE OF INVENTION:  Eicosanoid Formation
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Calfee, Halter & Griwold LLP
;      STREET:  800 Superior Avenue
;      CITY:  Cleveland
;      STATE:  Ohio
;      COUNTRY:  USA
;      ZIP:  44114
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/627,254C
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Golrick, Mary E
;      REGISTRATION NUMBER:  34,829
;      REFERENCE/DOCKET NUMBER:  18525/00107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (216) 622-8200
;      TELEFAX:  (216) 241-0816
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
```

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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ANTI-SENSE:  YES
US-08-627-254C-16


  Query Match             89.5%;  Score 17;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATC 17
          |||||||||||||||||
Db      2 GGGCGCGGGCGAGCATC 18


RESULT  13
US-08-930-589A-19/c
; Sequence 19, Application US/08930589A
; Patent No. 6107087
;  GENERAL INFORMATION:
;    APPLICANT:  MERCK FROSST CANADA & CO.
;    APPLICANT:  O'NEILL, GARY P.
;    APPLICANT:  MANCINI, JOSEPH A.
;    TITLE OF INVENTION:  HIGH LEVEL EXPRESSION OF HUMAN
;    TITLE OF INVENTION:  CYCLOOXYGENASE-2
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merck & Co., Inc.
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/930,589A
;      FILING DATE:  28-JUN-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coppola, Joseph A
;      REGISTRATION NUMBER:  38,413
;      REFERENCE/DOCKET NUMBER:  19029PC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  732-594-6734
;      TELEFAX:  732-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3387 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-930-589A-19


  Query Match             89.5%;  Score 17;  DB 4;  Length 3387;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATC 17
          |||||||||||||||||
Db    113 GGGCGCGGGCGAGCATC 97


RESULT  14
US-08-930-589A-14/c
; Sequence 14, Application US/08930589A
; Patent No. 6107087
;  GENERAL INFORMATION:
;    APPLICANT:  MERCK FROSST CANADA & CO.
;    APPLICANT:  O'NEILL, GARY P.
;    APPLICANT:  MANCINI, JOSEPH A.
;    TITLE OF INVENTION:  HIGH LEVEL EXPRESSION OF HUMAN
;    TITLE OF INVENTION:  CYCLOOXYGENASE-2
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merck & Co., Inc.
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/930,589A
;      FILING DATE:  28-JUN-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coppola, Joseph A
;      REGISTRATION NUMBER:  38,413
;      REFERENCE/DOCKET NUMBER:  19029PC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  732-594-6734
;      TELEFAX:  732-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-930-589A-14


  Query Match             84.2%;  Score 16;  DB 4;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCAT 16
          ||||||||||||||||
Db     17 GGGCGCGGGCGAGCAT 2


RESULT  15
US-08-221-750A-2/c
; Sequence 2, Application US/08221750A
; Patent No. 5643747
;  GENERAL INFORMATION:
;    APPLICANT:  Baker, Steven M.
;    APPLICANT:  Deich, Robert A.
;    TITLE OF INVENTION:  Genes for the Export of Pertussis
;    TITLE OF INVENTION:  Holotoxin
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
```

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;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,750A
;      FILING DATE:  31-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/031,619
;      FILING DATE:  15-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carroll, Alice O.
;      REGISTRATION NUMBER:  33,542
;      REFERENCE/DOCKET NUMBER:  ACC93-01A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2472 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2472
US-08-221-750A-2


  Query Match             83.2%;  Score 15.8;  DB 1;  Length 2472;
  Best Local Similarity   89.5%;  Pred. No. 38;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           | ||||| ||||||||||| |
Db    1627 GAGCGCGCGCGAGCATCGC 1609


Search completed: April 20, 2001, 00:03:44
Job time: 9681 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 03:21:21 ; Search time 11165 Seconds
(without alignments)
8.860 Million cell updates/sec

Title: US-09-016-464-17
Perfect score: 19
Sequence: 1 GGGCGCGGGCGAGCATCGC 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13168883 seqs, 2603265903 residues

Total number of hits satisfying chosen parameters: 26337766

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
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2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	19	100.0	19	14	US-09-016-464-17	Sequence 17, Appl
c 3	19	100.0	23	3	US-07-994-760-8	Sequence 8, Appli
c 4	19	100.0	23	4	US-08-084-033A-8	Sequence 8, Appli
c 5	19	100.0	23	13	US-08-930-589-8	Sequence 8, Appli
c 6	19	100.0	23	22	US-09-599-781-8	Sequence 8, Appli
c 7	19	100.0	159	1	PCT-US00-30888-11	Sequence 11, Appl
c 8	19	100.0	159	1	PCT-US00-30888A-11	Sequence 11, Appl
c 9	19	100.0	159	18	US-09-437-457-11	Sequence 11, Appl
c 10	19	100.0	159	18	US-09-437-458-11	Sequence 11, Appl
c 11	19	100.0	159	29	US-09-729-447-11	Sequence 11, Appl
c 12	19	100.0	219	25	US-09-652-918-2902	Sequence 2902, Ap
c 13	19	100.0	227	25	US-09-652-816-6526	Sequence 6526, Ap
c 14	19	100.0	284	28	US-09-716-990-85	Sequence 85, Appl
c 15	19	100.0	346	17	US-09-396-087-2011	Sequence 2011, Ap
c 16	19	100.0	349	25	US-09-644-869-5749	Sequence 5749, Ap
c 17	19	100.0	374	29	US-09-726-809-2115	Sequence 2115, Ap
c 18	19	100.0	375	25	US-09-652-128-4892	Sequence 4892, Ap
c 19	19	100.0	381	29	US-09-726-809-1224	Sequence 1224, Ap
c 20	19	100.0	389	29	US-09-726-809-2204	Sequence 2204, Ap
c 21	19	100.0	390	25	US-09-652-915-6360	Sequence 6360, Ap
c 22	19	100.0	394	25	US-09-652-915-6254	Sequence 6254, Ap
c 23	19	100.0	403	25	US-09-652-816-6600	Sequence 6600, Ap
c 24	19	100.0	403	25	US-09-652-918-2324	Sequence 2324, Ap
c 25	19	100.0	403	29	US-09-726-810-516	Sequence 516, App
c 26	19	100.0	407	28	US-09-710-286-1462	Sequence 1462, Ap
c 27	19	100.0	421	29	US-09-721-588-2251	Sequence 2251, Ap
c 28	19	100.0	423	29	US-09-726-809-1444	Sequence 1444, Ap
c 29	19	100.0	424	29	US-09-726-810-1474	Sequence 1474, Ap
c 30	19	100.0	429	19	US-09-502-330-324	Sequence 324, App
c 31	19	100.0	429	25	US-09-641-638-324	Sequence 324, App
c 32	19	100.0	430	29	US-09-726-810-715	Sequence 715, App
c 33	19	100.0	431	28	US-09-716-990-210	Sequence 210, App
c 34	19	100.0	431	29	US-09-726-810-2251	Sequence 2251, Ap
c 35	19	100.0	445	25	US-09-644-869-7132	Sequence 7132, Ap
c 36	19	100.0	457	25	US-09-652-128-4340	Sequence 4340, Ap
c 37	19	100.0	462	29	US-09-726-809-1946	Sequence 1946, Ap
c 38	19	100.0	464	29	US-09-726-810-1436	Sequence 1436, Ap
c 39	19	100.0	467	17	US-09-396-087-985	Sequence 985, App
c 40	19	100.0	468	25	US-09-652-918-2292	Sequence 2292, Ap
c 41	19	100.0	469	28	US-09-710-286-1461	Sequence 1461, Ap
c 42	19	100.0	471	28	US-09-710-286-1903	Sequence 1903, Ap
c 43	19	100.0	472	28	US-09-716-990-483	Sequence 483, App
c 44	19	100.0	481	25	US-09-649-162-4790	Sequence 4790, Ap
c 45	19	100.0	482	18	US-09-432-241A-2676	Sequence 2676, Ap

ALIGNMENTS

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RESULT   1
US-08-474-497-17
; Sequence 17, Application US/08474497
;  GENERAL INFORMATION:
;    APPLICANT:  Nyce, Jonathan W.
;    TITLE OF INVENTION:  Method of Treatment of Lung Diseases
;    TITLE OF INVENTION:  Using Antisense Oligonucleotides
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  Post Office Drawer 34009
;      CITY:  Charlotte
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,497
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5218-32
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 881-3140
;      TELEFAX:  (919) 881-3175
;      TELEX:  575102
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  12
;      OTHER INFORMATION:  /standard_name= "Reduced A"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  15
;      OTHER INFORMATION:  /standard_name= "Reduced A"
US-08-474-497-17


  Query Match             100.0%;  Score 19;  DB 8;  Length 19;
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
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Db      1 GGGCGCGGGCGAGCATCGC 19


RESULT   2
US-09-016-464-17
; Sequence 17, Application US/09016464
;   GENERAL INFORMATION:
;        APPLICANT: Nyce, Jonathan W.
;        TITLE OF INVENTION: Method of Treatment of Lung Diseases
;                            Using Antisense Oligonucleotides
;        NUMBER OF SEQUENCES: 44
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Kenneth D. Sibley
;             STREET: Post Office Drawer 34009
;             CITY: Charlotte
;             STATE: NC
;             COUNTRY: USA
;             ZIP: 28234
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/016,464
;             FILING DATE: 30-Jan-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/474,497
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sibley, Kenneth D.
;             REGISTRATION NUMBER: 31,665
;             REFERENCE/DOCKET NUMBER: 5218-32
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (919) 881-3140
;             TELEFAX: (919) 881-3175
;             TELEX: 575102
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 19 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  12
;             OTHER INFORMATION:  /standard_name= "Reduced A"
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  15
;             OTHER INFORMATION:  /standard_name= "Reduced A"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-016-464-17


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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db      1 GGGCGCGGGCGAGCATCGC 19


RESULT   3
US-07-994-760-8/c
; Sequence 8, Application US/07994760
;  GENERAL INFORMATION:
;    APPLICANT:  Kennedy, Brian P.
;    APPLICANT:  Cromlish, Wanda
;    APPLICANT:  O'Neill, Gary
;    APPLICANT:  Vickers, Philip J.
;    APPLICANT:  Wong, Elizabeth
;    TITLE OF INVENTION:  HUMAN CYCLOOXYGENASE-2 cDNA AND
;    TITLE OF INVENTION:  ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merck & Co., Inc.
;      STREET:  126 Lincoln Avenue
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      COMPUTER:  Macintosh IIci
;      OPERATING SYSTEM:  Macintosh
;      SOFTWARE:  Microsoftword 5.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/994,760
;      FILING DATE:  19921222
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Panzer, Curtis C.
;      REGISTRATION NUMBER:  33,752
;      REFERENCE/DOCKET NUMBER:  18906
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-3199
;      TELEFAX:  (908)594-4720
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-994-760-8


  Query Match           100.0%;  Score 19;  DB 3;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db     21 GGGCGCGGGCGAGCATCGC 3


RESULT   4
US-08-084-033A-8/c
; Sequence 8, Application US/08084033A
;  GENERAL INFORMATION:
;    APPLICANT:  O'NEILL, GARY P
;    APPLICANT:  MANCINI, JOSEPH A
;    TITLE OF INVENTION:  HIGH LEVEL EXPRESSION OF HUMAN
;    TITLE OF INVENTION:  CYCLOOXYGENASE-2
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHRISTINE E CARTY
;      STREET:  P.O. BOX 2000, 126 E. LINCOLN AVE.
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/084,033A
;      FILING DATE:  28-JUN-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARTY, CHRISTINE E
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  19029
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-6734
;      TELEFAX:  908-594-4720
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-084-033A-8


  Query Match           100.0%;  Score 19;  DB 4;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db     21 GGGCGCGGGCGAGCATCGC 3


RESULT   5
US-08-930-589-8/c
; Sequence 8, Application US/08930589
;  GENERAL INFORMATION:
;    APPLICANT:  MERCK FROSST CANADA & CO.
;    APPLICANT:  O'NEILL, GARY P
;    APPLICANT:  MANCINI, JOSEPH A
;    TITLE OF INVENTION:  HIGH LEVEL EXPRESSION OF HUMAN
;    TITLE OF INVENTION:  CYCLOOXYGENASE-2
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MERCK & CO., INC.
;      STREET:  P. O. BOX 2000 - 126 E. LINCOLN AVE.
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/930,589
;      FILING DATE:  28-JUN-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COPPOLA, JOSEPH A.
;      REGISTRATION NUMBER:  38,413
;      REFERENCE/DOCKET NUMBER:  19029PC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  732-594-6734
;      TELEFAX:  732-594-4720
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-930-589-8


  Query Match           100.0%;  Score 19;  DB 13;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db     21 GGGCGCGGGCGAGCATCGC 3


RESULT   6
US-09-599-781-8/c
; Sequence 8, Application US/09599781
;   GENERAL INFORMATION:
;        APPLICANT: MERCK FROSST CANADA & CO.
;                   O'NEILL, GARY P.
;                   MANCINI, JOSEPH A.
;        TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
;                            CYCLOOXYGENASE-2
;        NUMBER OF SEQUENCES: 23
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;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Merck & Co., Inc.
;            STREET: P.O. Box 2000, 126 E. Lincoln Ave.
;            CITY: Rahway
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 07065-0900
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows
;            SOFTWARE: FastSEQ for Windows Version 2.0b
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/599,781
;            FILING DATE: 21-Jun-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/084,033
;            FILING DATE: 27-Sep-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Coppola, Joseph A
;            REGISTRATION NUMBER: 38,413
;            REFERENCE/DOCKET NUMBER: 19029PC
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 732-594-6734
;            TELEFAX: 732-594-4720
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 23 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-599-781-8


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  Best Local Similarity  100.0%;  Pred. No. 1.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||||||||
Db     21 GGGCGCGGGCGAGCATCGC 3


RESULT   7
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; Sequence 11, Application PC/TUS0030888
; GENERAL INFORMATION:
;  APPLICANT:  Message Pharmaceuticals, Inc.
;  TITLE OF INVENTION:  NUCLEIC ACID SEQUENCES AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
;  TITLE OF INVENTION:  INTERACTIONS AND MRNA FUNCTIONALITY
;  FILE REFERENCE:  50093/014W01
;  CURRENT APPLICATION NUMBER: PCT/US00/30888
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER:  09/437,458
;  PRIOR FILING DATE:  1999-11-10
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 159
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US00-30888-11


  Query Match           100.0%;  Score 19;  DB 1;  Length 159;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
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RESULT   8
PCT-US00-30888A-11/c
; Sequence 11, Application PC/TUS0030888A
; GENERAL INFORMATION:
;  APPLICANT:  Message Pharmaceuticals, Inc.
;  TITLE OF INVENTION:  NUCLEIC ACID SEQUENCES AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
;  TITLE OF INVENTION:  INTERACTIONS AND MRNA FUNCTIONALITY
;  FILE REFERENCE:  50093/014W01
;  CURRENT APPLICATION NUMBER: PCT/US00/30888A
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER:  09/437,458
;  PRIOR FILING DATE:  1999-11-10
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 159
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US00-30888A-11


  Query Match           100.0%;  Score 19;  DB 1;  Length 159;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||||||||
Db    113 GGGCGCGGGCGAGCATCGC 95


RESULT   9
US-09-437-457-11/c
; Sequence 11, Application US/09437457
; GENERAL INFORMATION:
;  APPLICANT: Giordano, Anthony
;  APPLICANT: Xavier, Ashish
;  TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND METHODS FOR
;  TITLE OF INVENTION: IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
;  TITLE OF INVENTION: INTERACTIONS AND MRNA FUNCTIONALITY
;  FILE REFERENCE: 50093/014001
;  CURRENT APPLICATION NUMBER: US/09/437,457
;  CURRENT FILING DATE: 1999-11-10
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 159
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-437-457-11


  Query Match           100.0%;  Score 19;  DB 18;  Length 159;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||||||||
Db    113 GGGCGCGGGCGAGCATCGC 95


RESULT  10
US-09-437-458-11/c
; Sequence 11, Application US/09437458
; GENERAL INFORMATION:
;  APPLICANT: Giordano, Anthony
;  APPLICANT: Xavier, Ashish
;  TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND METHODS FOR
```

```
;  TITLE OF INVENTION: IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
;  TITLE OF INVENTION: INTERACTIONS AND MRNA FUNCTIONALITY
;  FILE REFERENCE: 50093/014001
;  CURRENT APPLICATION NUMBER: US/09/437,458
;  CURRENT FILING DATE: 1999-11-10
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 159
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-437-458-11


  Query Match            100.0%;  Score 19;  DB 18;  Length 159;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db    113 GGGCGCGGGCGAGCATCGC 95


RESULT  11
US-09-729-447-11/c
; Sequence 11, Application US/09729447
; GENERAL INFORMATION:
;  APPLICANT: Giordano, Anthony
;  APPLICANT:  Xavier, Ashish
;  TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
;  TITLE OF INVENTION:  INTERACTIONS AND MRNA FUNCTIONALITY
;  FILE REFERENCE: 50093/014001
;  CURRENT APPLICATION NUMBER: US/09/729,447
;  CURRENT FILING DATE:  2000-12-04
;  PRIOR APPLICATION NUMBER: 09/437,458
;  PRIOR FILING DATE: 1999-11-10
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 159
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-729-447-11


  Query Match            100.0%;  Score 19;  DB 29;  Length 159;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db    113 GGGCGCGGGCGAGCATCGC 95


RESULT  12
US-09-652-918-2902/c
; Sequence 2902, Application US/09652918
; GENERAL INFORMATION:
;  APPLICANT:  Galvin, Katherine
;  APPLICANT:  Holtzman, Douglas A.
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.1187-001
;  CURRENT APPLICATION NUMBER: US/09/652,918
;  CURRENT FILING DATE:  2000-08-30
;  PRIOR APPLICATION NUMBER:  60/151,130
;  PRIOR FILING DATE:  1999-08-30
;  NUMBER OF SEQ ID NOS:  8985
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 2902
;   LENGTH: 219
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(219)
;   OTHER INFORMATION: n = A,T,C or G
US-09-652-918-2902


  Query Match            100.0%;  Score 19;  DB 25;  Length 219;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db    148 GGGCGCGGGCGAGCATCGC 130


RESULT  13
US-09-652-816-6526/c
; Sequence 6526, Application US/09652816
; GENERAL INFORMATION:
;  APPLICANT:  Gutierrez-Ramos, Jose-Carlos
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.1177-001
;  CURRENT APPLICATION NUMBER: US/09/652,816
;  CURRENT FILING DATE:  2000-08-31
;  PRIOR APPLICATION NUMBER:  60/152,111
;  PRIOR FILING DATE:  1999-08-31
;  NUMBER OF SEQ ID NOS:  9647
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 6526
;   LENGTH: 227
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-652-816-6526


  Query Match            100.0%;  Score 19;  DB 25;  Length 227;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          |||||||||||||||||||
Db    164 GGGCGCGGGCGAGCATCGC 146


RESULT  14
US-09-716-990-85/c
; Sequence 85, Application US/09716990
; GENERAL INFORMATION:
;  APPLICANT:  Gearing, David P.
;  APPLICANT:  Holtzman, Douglas A.
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.2039-001
;  CURRENT APPLICATION NUMBER: US/09/716,990
;  CURRENT FILING DATE:  2000-11-21
;  PRIOR APPLICATION NUMBER:  US 60/166,926
;  PRIOR FILING DATE:  1999-11-22
;  NUMBER OF SEQ ID NOS:  1691
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 85
;   LENGTH: 284
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(284)
;   OTHER INFORMATION: n = A,T,C or G
US-09-716-990-85
```

```
  Query Match             100.0%;  Score 19;  DB 28;  Length 284;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           |||||||||||||||||||
Db     147 GGGCGCGGGCGAGCATCGC 129


RESULT  15
US-09-396-087-2011/c
; Sequence 2011, Application US/09396087
; GENERAL INFORMATION:
;  APPLICANT: Gearing, David P.
;  APPLICANT: Holtzman, Douglas A.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
;  TITLE OF INVENTION: PULMONARY ARTERY SMOOTH MUSCLE LIBRARY
;  FILE REFERENCE: MLN98-39pM
;  CURRENT APPLICATION NUMBER: US/09/396,087
;  CURRENT FILING DATE: 1999-09-14
;  EARLIER APPLICATION NUMBER: 60/100,260
;  EARLIER FILING DATE: 1998-09-14
;  EARLIER APPLICATION NUMBER: 60/107,226
;  EARLIER FILING DATE: 1998-11-05
;  EARLIER APPLICATION NUMBER: 60/131,810
;  EARLIER FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 5220
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2011
;   LENGTH: 346
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(346)
;   OTHER INFORMATION: n = A,T,C or G
US-09-396-087-2011


  Query Match             100.0%;  Score 19;  DB 17;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCGC 19
           |||||||||||||||||||
Db     139 GGGCGCGGGCGAGCATCGC 121


Search completed: April 20, 2001, 03:21:23
Job time: 14170 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:15:36 ; Search time 101.94 Seconds
(without alignments)
25.791 Million cell updates/sec

Title: US-09-016-464-17
Perfect score: 19
Sequence: 1 GGGCGCGGGCGAGCATCGC 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 46985 seqs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	19	100.0	3387	5	US-09-543-679A-2682	Sequence 2682, Ap
c	2	19	100.0	15240	5	US-09-543-679A-2684	Sequence 2684, Ap
c	3	17	89.5	9453	5	US-09-543-679A-2683	Sequence 2683, Ap
	4	15.8	83.2	19	5	US-09-543-679A-1052	Sequence 1052, Ap
	5	15.8	83.2	60	5	US-09-543-679A-1054	Sequence 1054, Ap
	6	15.8	83.2	101	5	US-09-543-679A-1729	Sequence 1729, Ap
	7	15.8	83.2	6225	5	US-09-543-679A-2410	Sequence 2410, Ap
	8	15.8	83.2	35459	5	US-09-543-679A-3003	Sequence 3003, Ap
c	9	14.8	77.9	267	5	US-09-739-449-6823	Sequence 6823, Ap
c	10	14.8	77.9	555	5	US-09-739-449-5546	Sequence 5546, Ap
c	11	14.8	77.9	1725	6	US-60-248-505-1976	Sequence 1976, Ap
c	12	14.8	77.9	3286	6	US-60-248-505-1617	Sequence 1617, Ap
	13	14.8	77.9	26297	6	US-60-248-505-644	Sequence 644, App
	14	14.8	77.9	68618	6	US-60-248-505-35	Sequence 35, Appl
	15	14.8	77.9	68619	6	US-60-248-505-500	Sequence 500, App
	16	14.8	77.9	124647	6	US-60-248-505-285	Sequence 285, App
	17	14.8	77.9	318095	5	US-09-739-449-215	Sequence 215, App
	18	14.8	77.9	506113	5	US-09-739-449-218	Sequence 218, App
	19	14.4	75.8	588	1	PCT-US01-09217-18	Sequence 18, Appl
	20	14.4	75.8	588	5	US-09-816-523-18	Sequence 18, Appl
	21	14.4	75.8	1479	5	US-09-739-449-7339	Sequence 7339, Ap
c	22	14.4	75.8	17138	5	US-09-813-819-3	Sequence 3, Appli
	23	14.4	75.8	20310	5	US-09-739-449-191	Sequence 191, App
	24	14.2	74.7	460	5	US-09-813-206-701	Sequence 701, App
c	25	14.2	74.7	465	5	US-09-809-391-77	Sequence 77, Appl
	26	14.2	74.7	612	5	US-09-739-449-6998	Sequence 6998, Ap
	27	14.2	74.7	615	5	US-09-739-449-6910	Sequence 6910, Ap
	28	14.2	74.7	729	5	US-09-739-449-2486	Sequence 2486, Ap
	29	14.2	74.7	774	5	US-09-739-449-6848	Sequence 6848, Ap
	30	14.2	74.7	1033	5	US-09-813-206-700	Sequence 700, App
	31	14.2	74.7	1068	5	US-09-813-206-18	Sequence 18, Appl
c	32	14.2	74.7	1074	5	US-09-739-449-5334	Sequence 5334, Ap
c	33	14.2	74.7	1158	5	US-09-739-449-4688	Sequence 4688, Ap
	34	14.2	74.7	1159	5	US-09-813-206-20	Sequence 20, Appl
	35	14.2	74.7	2223	1	PCT-US01-09226-28	Sequence 28, Appl
	36	14.2	74.7	2265	5	US-09-739-449-4875	Sequence 4875, Ap
	37	14.2	74.7	2343	5	US-09-739-449-7491	Sequence 7491, Ap
c	38	14.2	74.7	2467	5	US-09-739-449-5894	Sequence 5894, Ap
	39	14.2	74.7	2664	5	US-09-739-449-4873	Sequence 4873, Ap
c	40	14.2	74.7	3008	1	PCT-US01-01350-298	Sequence 298, App
	41	14.2	74.7	3296	5	US-09-423-844-309	Sequence 309, App
	42	14.2	74.7	3753	1	PCT-US01-09226-29	Sequence 29, Appl
	43	14.2	74.7	4629	5	US-09-739-449-7069	Sequence 7069, Ap
	44	14.2	74.7	29171	6	US-60-248-505-258	Sequence 258, App
	45	14.2	74.7	29172	6	US-60-248-505-462	Sequence 462, App

ALIGNMENTS

```
RESULT   1
US-09-543-679A-2682/c
; Sequence 2682, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2682:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 3387 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2682
US-09-543-679A-2682


  Query Match             100.0%;  Score 19;  DB 5;  Length 3387;
  Best Local Similarity   100.0%;  Pred. No. 0.32;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||||||||
Db    113 GGGCGCGGGCGAGCATCGC 95


RESULT   2
US-09-543-679A-2684/c
; Sequence 2684, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2684:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15240 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2684
US-09-543-679A-2684


  Query Match             100.0%;  Score 19;  DB 5;  Length 15240;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||||||||||||
Db   2513 GGGCGCGGGCGAGCATCGC 2495


RESULT   3
US-09-543-679A-2683/c
; Sequence 2683, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2683:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9453 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2683
US-09-543-679A-2683


  Query Match             89.5%;  Score 17;  DB 5;  Length 9453;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATC 17
          |||||||||||||||||
Db    981 GGGCGCGGGCGAGCATC 965


RESULT   4
US-09-543-679A-1052
; Sequence 1052, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
```

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;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1052:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 19 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: Genomic DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1052:
US-09-543-679A-1052


  Query Match             83.2%;  Score 15.8;  DB 5;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 20;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||| || ||||
Db      1 GGGCGCGGGCGBGCBTCGC 19


RESULT   5
US-09-543-679A-1054
; Sequence 1054, Application US/09543679A
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1054:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 60 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: Genomic DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1054:
US-09-543-679A-1054


  Query Match             83.2%;  Score 15.8;  DB 5;  Length 60;
  Best Local Similarity   89.5%;  Pred. No. 17;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||| || ||||
Db     28 GGGCGCGGGCGBGCBTCGC 46


RESULT   6
US-09-543-679A-1729
; Sequence 1729, Application US/09543679A
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1729:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 101 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1729:
US-09-543-679A-1729


  Query Match             83.2%;  Score 15.8;  DB 5;  Length 101;
  Best Local Similarity   89.5%;  Pred. No. 16;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||| || ||||
Db      1 GGGCGCGGGCGBGCBTCGC 19


RESULT   7
US-09-543-679A-2410
; Sequence 2410, Application US/09543679A
;   GENERAL INFORMATION:
```

```
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2410:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 6225 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2410:
US-09-543-679A-2410


  Query Match             83.2%;  Score 15.8;  DB 5;  Length 6225;
  Best Local Similarity   89.5%;  Pred. No. 8.8;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||| || ||||
Db    313 GGGCGCGGGCGBGCBTCGC 331


RESULT   8
US-09-543-679A-3003
; Sequence 3003, Application US/09543679A
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3003:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 35459 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3003:
US-09-543-679A-3003


  Query Match             83.2%;  Score 15.8;  DB 5;  Length 35459;
  Best Local Similarity   89.5%;  Pred. No. 6.8;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGGCGCGGGCGAGCATCGC 19
          ||||||||||| || ||||
Db    313 GGGCGCGGGCGBGCBTCGC 331


RESULT   9
US-09-739-449-6823/c
; Sequence 6823, Application US/09739449
; GENERAL INFORMATION:
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15490)C
;  CURRENT APPLICATION NUMBER: US/09/739,449
;  CURRENT FILING DATE:  2000-12-19
;  PRIOR APPLICATION NUMBER: US 09/514,000
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 6823
;   LENGTH: 267
;   TYPE: DNA
;   ORGANISM: Agrobacterium tumefaciens
US-09-739-449-6823


  Query Match             77.9%;  Score 14.8;  DB 5;  Length 267;
  Best Local Similarity   88.9%;  Pred. No. 40;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 GGCGCGGGCGAGCATCGC 19
          |||||||||| | |||||
Db    264 GGCGCGGGCGCGGATCGC 247


RESULT  10
US-09-739-449-5546/c
; Sequence 5546, Application US/09739449
; GENERAL INFORMATION:
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15490)C
;  CURRENT APPLICATION NUMBER: US/09/739,449
```

```
;  CURRENT FILING DATE:  2000-12-19
;  PRIOR APPLICATION NUMBER: US 09/514,000
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 5546
;   LENGTH: 555
;   TYPE: DNA
;   ORGANISM: Agrobacterium tumefaciens
US-09-739-449-5546


  Query Match            77.9%;  Score 14.8;  DB 5;  Length 555;
  Best Local Similarity   88.9%;  Pred. No. 36;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GGCGCGGGCGAGCATCGC 19
           |||| || ||||||||||
Db     312 GGCGGGGCCGAGCATCGC 295


RESULT  11
US-60-248-505-1976/c
; Sequence 1976, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: c1000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1976
;   LENGTH: 1725
;   TYPE: DNA
;   ORGANISM: Human
US-60-248-505-1976


  Query Match            77.9%;  Score 14.8;  DB 6;  Length 1725;
  Best Local Similarity   88.9%;  Pred. No. 31;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GGCGCGGGCGAGCATCGC 19
           ||| ||||||||||| |||
Db     513 GGCCCGGGCGAGCAGCGC 496


RESULT  12
US-60-248-505-1617/c
; Sequence 1617, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: c1000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1617
;   LENGTH: 3286
;   TYPE: DNA
;   ORGANISM: Human
US-60-248-505-1617


  Query Match            77.9%;  Score 14.8;  DB 6;  Length 3286;
  Best Local Similarity   88.9%;  Pred. No. 28;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GGCGCGGGCGAGCATCGC 19
           ||| ||||||||||| |||
Db    1161 GGCCCGGGCGAGCAGCGC 1144


RESULT  13
US-60-248-505-644
; Sequence 644, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: c1000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 644
;   LENGTH: 26297
;   TYPE: DNA
;   ORGANISM: human
US-60-248-505-644


  Query Match            77.9%;  Score 14.8;  DB 6;  Length 26297;
  Best Local Similarity   88.9%;  Pred. No. 21;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GGCGCGGGCGAGCATCGC 19
           ||| ||||||||||| |||
Db  15013 ggcccgggcgagcagcgc 15030


RESULT  14
US-60-248-505-35
; Sequence 35, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: c1000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
;   LENGTH: 68618
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(68618)
;   OTHER INFORMATION: n = A,T,C or G
US-60-248-505-35


  Query Match            77.9%;  Score 14.8;  DB 6;  Length 68618;
  Best Local Similarity   88.9%;  Pred. No. 18;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCG 18
           || |||||||| ||||||
Db  53760 ggccgcgggcgcgcatcg 53777


RESULT  15
US-60-248-505-500
; Sequence 500, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
```

```
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: cl000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 500
;   LENGTH: 68619
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(68619)
;   OTHER INFORMATION: n = A,T,C or G
US-60-248-505-500


  Query Match            77.9%;  Score 14.8;  DB 6;  Length 68619;
  Best Local Similarity  88.9%;  Pred. No. 18;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GGGCGCGGGCGAGCATCG 18
           || |||||||| ||||||
Db   53761 ggccgcgggcgcgcatcg 53778


Search completed: April 20, 2001, 00:15:40
Job time: 9477 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:00:25 ; Search time 2028.86 Seconds
(without alignments)
63.738 Million cell updates/sec

Title: US-09-016-464-18
Perfect score: 21
Sequence: 1 CCTCCTTCCTGGTCTGTCTGC 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
16: em_ba1:*
17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
21: em_htgo_rod:*
22: em_htg_hum1:*
23: em_htg_hum2:*
24: em_htg_hum3:*
25: em_htg_hum4:*
26: em_htg_hum5:*
27: em_htg_hum6:*
28: em_htg_hum7:*
29: em_htg_hum8:*
30: em_htg_inv1:*
31: em_htg_inv2:*
32: em_htg_other:*
33: em_htg_rod:*
34: em_hum1:*
35: em_hum2:*
36: em_hum3:*
37: em_hum4:*
38: em_hum5:*
39: em_hum6:*
40: em_hum7:*
41: em_in:*
42: em_om:*
43: em_or:*
44: em_ov:*
45: em_pat:*
46: em_ph:*
47: em_pl:*
48: em_ro:*
49: em_sts:*
50: em_sy:*
51: em_un:*
52: em_vi:*
53: gb_sts1:*
54: gb_sts2:*
55: gb_sts3:*
56: gb_sy:*
57: gb_un:*
58: gb_vi1:*
59: gb_vi2:*
60: gb_htg1:*
61: gb_htg2:*
62: gb_htg3:*
63: gb_htg4:*
64: gb_htg5:*
65: gb_htg6:*
66: gb_htg7:*
67: gb_htg8:*
68: gb_htg9:*
69: gb_htg10:*
70: gb_htg11:*
71: gb_htg12:*
72: gb_htg13:*
73: gb_htg14:*
74: gb_htg15:*
75: gb_htg16:*
76: gb_htg17:*
77: gb_htg18:*
78: gb_htg19:*
79: gb_htg20:*
80: gb_htg21:*
81: gb_htg22:*
82: gb_htg23:*
83: gb_htg24:*
84: gb_htg25:*
85: gb_pr1:*
86: gb_pr2:*
87: gb_pr3:*
88: gb_pr4:*
89: gb_pr5:*
90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_ro1:*
95: gb_ro2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	21	100.0	483	91	GGU24097	U24097 Gorilla gor
c 2	21	100.0	483	93	PTU24103	U24103 Pan troglod
c 3	21	100.0	715	92	HSECP	X15161 Human mRNA
c 4	21	100.0	718	93	HUMECPA	M28128 Homo sapien
c 5	21	100.0	1199	88	AF294027	AF294027 Pan trogl
c 6	21	100.0	1199	88	AF294028	AF294028 Pan trogl
c 7	21	100.0	1203	88	AF294019	AF294019 Homo sapi
c 8	21	100.0	1203	88	AF294020	AF294020 Homo sapi
c 9	21	100.0	1203	88	AF294021	AF294021 Homo sapi
c 10	21	100.0	1203	88	AF294022	AF294022 Homo sapi
c 11	21	100.0	1203	88	AF294023	AF294023 Homo sapi

c	12	21	100.0	1203	88	AF294024	AF294024 Homo sapi
c	13	21	100.0	1203	88	AF294025	AF294025 Homo sapi
c	14	21	100.0	1203	88	AF294026	AF294026 Homo sapi
c	15	21	100.0	1452	92	HSECP1	X16545 Human DNA f
c	16	21	100.0	1669	92	HSECPG	X55990 Human ECP g
	17	21	100.0	157981	83	CNS05TD4	AL355922 Homo sapi
c	18	21	100.0	162472	83	CNS01DUW	AL133371 Homo sapi
c	19	19.4	92.4	483	93	MFU24098	U24098 Macaca fasc
	20	19.4	92.4	152689	77	AC087102	AC087102 Rattus no
	21	18.4	87.6	618	54	G56653	G56653 SHGC-102053
c	22	18.4	87.6	98070	88	AC025463	AC025463 Homo sapi
c	23	18.4	87.6	151104	61	AC010250	AC010250 Homo sapi
	24	18.4	87.6	151408	61	AC010397	AC010397 Homo sapi
	25	18.4	87.6	153170	91	HS1103G7	AL034548 Human DNA
c	26	18.4	87.6	159920	86	AC008447	AC008447 Homo sapi
c	27	18.4	87.6	174788	83	CNS01DVU	AL136039 Homo sapi
	28	18.4	87.6	200078	63	AC012181	AC012181 Homo sapi
c	29	18.4	87.6	204405	66	AC021183	AC021183 Homo sapi
	30	18	85.7	138941	89	AL136528	AL136528 Human DNA
c	31	18	85.7	140084	81	AL390963	AL390963 Homo sapi
	32	18	85.7	150829	61	AC009092	AC009092 Homo sapi
	33	18	85.7	164919	69	AC024903	AC024903 Homo sapi
	34	18	85.7	168951	65	AC016927	AC016927 Homo sapi
	35	18	85.7	169391	66	AC021021	AC021021 Homo sapi
c	36	18	85.7	181104	61	AC009162	AC009162 Homo sapi
c	37	18	85.7	202872	64	AC016160	AC016160 Homo sapi
	38	18	85.7	207882	62	AC010674	AC010674 Homo sapi
c	39	17.8	84.8	482	53	AF192011	AF192011 Homo sapi
c	40	17.8	84.8	483	93	PPU24101	U24101 Pongo pygma
c	41	17.8	84.8	1032	53	CNS06LTE	AL404616 T7 end of
c	42	17.8	84.8	3583	93	HUMUBILP	J03589 Human ubiqu
c	43	17.8	84.8	3653	88	AF009356	AF009356 Homo sapi
	44	17.8	84.8	14180	94	MMU67065	U67065 Mus musculu
	45	17.8	84.8	38687	90	AL391690	AL391690 Human DNA

ALIGNMENTS

```
RESULT   1
GGU24097/c
LOCUS       GGU24097      483 bp    DNA             PRI       17-JUN-1995
DEFINITION  Gorilla gorilla eosinophil cationic protein gene, complete cds.
ACCESSION   U24097
VERSION     U24097.1  GI:790263
KEYWORDS    ribonuclease.
SOURCE      gorilla.
  ORGANISM  Gorilla gorilla
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
REFERENCE   1  (bases 1 to 483)
  AUTHORS   Rosenberg,H.F., Dyer,K.D., Tiffany,H.L. and Gonzalez,M.
  TITLE     Rapid evolution of a unique family of primate ribonuclease genes
  JOURNAL   Nature Genet. 10 (2), 219-223 (1995)
  MEDLINE   95392576
REFERENCE   2  (bases 1 to 483)
  AUTHORS   Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-APR-1995) Helene F. Rosenberg, Laboratory of Host
            Defenses, NIAID, National Institutes of Health, Building 10, Room
            11N104, 9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .483
                     /organism="Gorilla gorilla"
                     /db_xref="taxon:9593"
     sig_peptide     1. .81
     CDS             1. .483
                     /note="ribonuclease"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAC50143.1"
                     /db_xref="GI:790264"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRVINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCLHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPQDSPRYPVVPVHLDTTI
                     "
     mat_peptide     82. .480
                     /note="ribonuclease"
                     /product="eosinophil cationic protein"
BASE COUNT      126 a    120 c    101 g    136 t
ORIGIN
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  Query Match           100.0%;  Score 21;  DB 91;  Length 483;
  Best Local Similarity  100.0%;  Pred. No. 4.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    396 CCTCCTTCCTGGTCTGTCTGC 376
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```
RESULT   2
PTU24103/c
LOCUS       PTU24103      483 bp    DNA             PRI       17-JUN-1995
DEFINITION  Pan troglodytes eosinophil cationic protein gene, complete cds.
ACCESSION   U24103
VERSION     U24103.1  GI:790277
KEYWORDS    ribonuclease.
SOURCE      chimpanzee.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 483)
  AUTHORS   Rosenberg,H.F., Dyer,K.D., Tiffany,H.L. and Gonzalez,M.
  TITLE     Rapid evolution of a unique family of primate ribonuclease genes
  JOURNAL   Nature Genet. 10 (2), 219-223 (1995)
  MEDLINE   95392576
REFERENCE   2  (bases 1 to 483)
  AUTHORS   Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-APR-1995) Helene F. Rosenberg, Laboratory of Host
            Defenses, NIAID, National Institutes of Health, Building 10 Room
            11N104, 9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .483
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
     sig_peptide     1. .81
     CDS             1. .483
                     /note="ribonuclease"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAC50150.1"
                     /db_xref="GI:790278"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRVINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHQSR
                     FRVPLLHCDLINPGAQNISNCGYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     mat_peptide     82. .480
                     /note="ribonuclease"
                     /product="eosinophil cationic protein"
BASE COUNT      126 a    122 c    102 g    133 t
ORIGIN
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  Query Match           100.0%;  Score 21;  DB 93;  Length 483;
  Best Local Similarity  100.0%;  Pred. No. 4.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    396 CCTCCTTCCTGGTCTGTCTGC 376
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RESULT   3
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HSECP/c
LOCUS       HSECP         715 bp    mRNA            PRI       22-MAR-1995
DEFINITION  Human mRNA for eosinophil cationic protein ECP.
ACCESSION   X15161
VERSION     X15161.1  GI:31076
KEYWORDS    cytotoxin; eosinophil cationic protein; glycoprotein;
            helminthotoxin; matrix protein; neurotoxin; perforin; ribonuclease.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 715)
  AUTHORS   Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-1989) Rosenberg H.F., Beth Israel Hospital, 330
            Brookline Avenue, Boston MA 02215, USA
REFERENCE   2  (bases 1 to 715)
  AUTHORS   Rosenberg,H.F., Ackerman,S.J. and Tenen,D.G.
  TITLE     Human eosinophil cationic protein. Molecular cloning of a cytotoxin
            and helminthotoxin with ribonuclease activity
  JOURNAL   J. Exp. Med. 170 (1), 163-176 (1989)
  MEDLINE   89310354
FEATURES             Location/Qualifiers
     source          1. .715
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /tissue_type="peripheral blood granulocytes"
                     /cell_type="eosinophil"
                     /cell_line="HL-60"
                     /clone_lib="lambda gt11"
     mRNA            <1. .715
                     /note="ECP mRNA"
     sig_peptide     55. .135
                     /product="signal peptide ((AA -27 to -1)"
     CDS             55. .537
                     /note="ECP preprotein"
                     /codon_start=1
                     /protein_id="CAA33251.1"
                     /db_xref="GI:31077"
                     /db_xref="SWISS-PROT:P12724"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     mat_peptide     136. .534
                     /product="mature ECP (AA 1-133)"
     polyA_site      715
                     /note="polyA site"
BASE COUNT      185 a    199 c    141 g    190 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 92;  Length 715;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    450 CCTCCTTCCTGGTCTGTCTGC 430


RESULT   4
HUMECPA/c
LOCUS       HUMECPA       718 bp    mRNA            PRI       06-OCT-1994
DEFINITION  Homo sapiens eosinophil cationic protein (ECP) mRNA, complete cds.
ACCESSION   M28128
VERSION     M28128.1  GI:556199
KEYWORDS    ECP gene; eosinophil cationic protein; neurotoxin.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 718)
  AUTHORS   Barker,R.L., Loegering,D.A., Ten,R.M., Hamann,K.J., Pease,L.R. and
            Gleich,G.J.
  TITLE     Eosinophil cationic protein cDNA. Comparison with other toxic
            cationic proteins and ribonucleases
  JOURNAL   J. Immunol. 143 (3), 952-955 (1989)
  MEDLINE   89309773
COMMENT     On Oct 8, 1994 this sequence version replaced gi:341832.
FEATURES             Location/Qualifiers
     source          1. .718
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_line="mononuclear cord blood cells stimulated with
                     EL4 supernatants"
                     /cell_type="eosinophil"
                     /note="vector lambda ZAP"
     5'UTR           1. .52
     CDS             53. .535
                     /note="bp 302. .310, 326. .334, 407. .414 glycosylation site;
                     preprotein"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAA50283.1"
                     /db_xref="GI:556200"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     sig_peptide     53. .133
     mat_peptide     134. .532
                     /product="eosinophil cationic protein"
     3'UTR           536. .713
     polyA_signal    693. .698
BASE COUNT      187 a    197 c    144 g    190 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 93;  Length 718;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    448 CCTCCTTCCTGGTCTGTCTGC 428


RESULT   5
AF294027/c
LOCUS       AF294027     1199 bp    DNA             PRI       19-DEC-2000
DEFINITION  Pan troglodytes haplotype 1 eosinophil cationic protein (ECP) gene,
            complete cds.
ACCESSION   AF294027
VERSION     AF294027.1  GI:9954419
KEYWORDS    .
SOURCE      chimpanzee.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1199)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1199)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1199
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /haplotype="1"
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     mRNA            join(<209. .276,503. .1169)
                     /gene="ECP"
                     /product="eosinophil cationic protein"
     gene            <209. .1169
                     /gene="ECP"
     CDS             508. .990
                     /gene="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG09050.1"
                     /db_xref="GI:9954420"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRVINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHQSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDATI
                     "
BASE COUNT      308 a    305 c    292 g    294 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 88;  Length 1199;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    903 CCTCCTTCCTGGTCTGTCTGC 883


RESULT   6
AF294028/c
LOCUS       AF294028     1199 bp    DNA             PRI       19-DEC-2000
DEFINITION  Pan troglodytes haplotype 2 eosinophil cationic protein (ECP) gene,
            complete cds.
ACCESSION   AF294028
VERSION     AF294028.1  GI:9954421
KEYWORDS    .
SOURCE      chimpanzee.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1199)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1199)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1199
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /haplotype="2"
     mRNA            join(<209. .276,503. .1169)
                     /gene="ECP"
                     /product="eosinophil cationic protein"
     gene            <209. .1169
                     /gene="ECP"
     CDS             508. .990
                     /gene="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG09051.1"
                     /db_xref="GI:9954422"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRVINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHQSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDATI
                     "
BASE COUNT      308 a    306 c    292 g    293 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 88;  Length 1199;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    903 CCTCCTTCCTGGTCTGTCTGC 883


RESULT   7
AF294019/c
LOCUS       AF294019     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 1 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294019
VERSION     AF294019.1  GI:11139039
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="1"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31589.1"
                     /db_xref="GI:11139040"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCTYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      317 a    306 c    285 g    295 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    907 CCTCCTTCCTGGTCTGTCTGC 887


RESULT   8
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```
AF294020/c
LOCUS       AF294020     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 2 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294020
VERSION     AF294020.1  GI:11139041
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="2"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31590.1"
                     /db_xref="GI:11139042"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      318 a    303 c    287 g    295 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    907 CCTCCTTCCTGGTCTGTCTGC 887


RESULT  9
AF294021/c
LOCUS       AF294021     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 3 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294021
VERSION     AF294021.1  GI:11139043
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="3"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31591.1"
                     /db_xref="GI:11139044"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCTYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      317 a    305 c    286 g    295 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    907 CCTCCTTCCTGGTCTGTCTGC 887


RESULT  10
AF294022/c
LOCUS       AF294022     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 4 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294022
VERSION     AF294022.1  GI:11139045
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /haplotype="4"
     mRNA       join(209. .276,507. .1173)
                /product="eosinophil cationic protein"
     exon       209. .276
                /number=1
     5'UTR      join(209. .276,507. .511)
     intron     277. .506
                /number=1
     exon       507. .1173
                /number=2
     CDS        512. .994
                /note="ECP"
                /codon_start=1
                /product="eosinophil cationic protein"
                /protein_id="AAG31592.1"
                /db_xref="GI:11139046"
                /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                "
     3'UTR      995. .1173
BASE COUNT      317 a    304 c    287 g    295 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    907 CCTCCTTCCTGGTCTGTCTGC 887


RESULT  11
AF294023/c
LOCUS       AF294023     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 5 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294023
VERSION     AF294023.1  GI:11139047
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="5"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31593.1"
                     /db_xref="GI:11139048"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      316 a    304 c    287 g    296 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    907 CCTCCTTCCTGGTCTGTCTGC 887


RESULT  12
AF294024/c
LOCUS       AF294024     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 6 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294024
VERSION     AF294024.1  GI:11139049
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="6"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31594.1"
                     /db_xref="GI:11139050"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      317 a    303 c    287 g    296 t
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```
ORIGIN


  Query Match             100.0%;  Score 21;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    907 CCTCCTTCCTGGTCTGTCTGC 887


RESULT  13
AF294025/c
LOCUS       AF294025     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 7 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294025
VERSION     AF294025.1  GI:11139051
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="7"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31595.1"
                     /db_xref="GI:11139052"
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                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCTYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      317 a    304 c    286 g    296 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    907 CCTCCTTCCTGGTCTGTCTGC 887


RESULT  14
AF294026/c
LOCUS       AF294026     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 8 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294026
VERSION     AF294026.1  GI:11139053
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="8"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31596.1"
                     /db_xref="GI:11139054"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
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                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      316 a    305 c    287 g    295 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    907 CCTCCTTCCTGGTCTGTCTGC 887


RESULT  15
HSECP1/c
LOCUS       HSECP1       1452 bp    DNA             PRI       24-APR-1993
DEFINITION  Human DNA for eosinophil cationic protein ECP.
ACCESSION   X16545
VERSION     X16545.1  GI:31080
KEYWORDS    cytotoxin; eosinophil cationic protein; helminthotoxin; neurotoxin.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1452)
```

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  AUTHORS   Barker,R.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-SEP-1989) Barker R.L., Mayo Clinic and Foundation,
            401 Guggenheim, Rochester Minnesota 55905, U S A
REFERENCE   2  (bases 1 to 1452)
  AUTHORS   Hamann,K.J., Ten,R.M., Loegering,D.A., Jenkins,R.B., Heise,M.T.,
            Schad,C.R., Pease,L.R., Gleich,G.J. and Barker,R.L.
  TITLE     Structure and chromosome localization of the human
            eosinophil-derived neurotoxin and eosinophil cationic protein
            genes: evidence for intronless coding sequences in the ribonuclease
            gene superfamily
  JOURNAL   Genomics 7 (4), 535-546 (1990)
  MEDLINE   90353951
COMMENT     see X15161 for human ECP cDNA seq.
FEATURES             Location/Qualifiers
     source          1. .1452
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_type="eosinophil"
                     /cell_line="human fetal liver charon 4A."
                     /clone_lib="ATCC 37333"
     TATA_signal     225. .231
     exon            279. .320
                     /number=1
     mRNA            join(279. .320,551. .1217)
     intron          321. .550
                     /number=1
     exon            551. .1217
                     /number=2
     sig_peptide     556. .636
                     /product="signal peptide (AA -27 to -1)"
     CDS             556. .1038
                     /note="eosinophil cationic protein precursor"
                     /codon_start=1
                     /protein_id="CAA34545.1"
                     /db_xref="GI:31081"
                     /db_xref="SWISS-PROT:P12724"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     mat_peptide     637. .1035
                     /product="mat. eosinophil cationic protein (AA 1 - 133)"
     polyA_signal    1196. .1201
BASE COUNT      380 a    376 c    323 g    373 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 92;  Length 1452;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTGC 21
           |||||||||||||||||||||
Db     951 CCTCCTTCCTGGTCTGTCTGC 931



Search completed: April 20, 2001, 00:00:28
Job time: 9505 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:12:58 ; Search time 547.68 Seconds
(without alignments)
22.384 Million cell updates/sec

Title: US-09-016-464-18
Perfect score: 21
Sequence: 1 CCTCCTTCCTGGTCTGTCTGC 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	21	18	T76118	Human eosinophil c
	2	21	100.0	81	20	X54596	Eosinophil cationi
	3	21	100.0	81	21	F20165	Human eosinophil c
	4	21	100.0	81	21	A34043	Human adenosine re
c	5	21	100.0	715	21	F21294	Human low adenosin
c	6	21	100.0	715	21	A35172	Human adenosine re
c	7	21	100.0	718	21	F21293	Human low adenosin
c	8	21	100.0	718	21	A35171	Human adenosine re
c	9	21	100.0	1452	21	F21295	Human low adenosin
c	10	21	100.0	1452	21	A35173	Human adenosine re
c	11	21	100.0	2885	21	F21296	Human low adenosin
c	12	21	100.0	2885	21	A35174	Human adenosine re
	13	21	100.0	7033	21	F20844	Human low adenosin
	14	21	100.0	7033	21	A34722	Human adenosine re
	15	21	100.0	7036	20	X55274	Human factor-relat
	16	21	100.0	114955	20	X53491	Human adenosine A1
	17	21	100.0	209273	21	F21437	Human factor-relat
	18	17.8	84.8	14180	19	V05159	Mouse butyrophilin
	19	17.4	82.9	262	18	X83217	Breast cancer tumo
	20	17.4	82.9	262	19	V68816	DNA molecule encod
	21	17.4	82.9	262	21	C80740	Human breast tumou
	22	16.8	80.0	585	20	X97764	Extended human sec
	23	16.8	80.0	1446	21	C73870	Human secreted pro
	24	16.8	80.0	2088	20	V68453	Human guanine nucl
	25	16.8	80.0	2178	20	V68451	Human guanine nucl
	26	16.8	80.0	2335	21	A47618	KCNQ4 Potassium ch
c	27	16.2	77.1	328	21	A93845	TADG-12V (truncate
	28	16.2	77.1	467	21	C28112	Human secreted pro
	29	16.2	77.1	735	21	C75784	Human ORFX ORF1339
c	30	16.2	77.1	775	18	T95759	Arabidopsis SCAREC
c	31	16.2	77.1	775	21	C65292	Arabidopsis SCLa10
c	32	16.2	77.1	2096	21	C50354	Arabidopsis thalia
c	33	16.2	77.1	2313	21	Z94095	Haematopoietic ste
	34	16.2	77.1	2394	21	C64285	Human membrane-ass
c	35	16.2	77.1	2544	21	A93843	Tumour associated
c	36	16.2	77.1	3517	17	T31287	Rabbit poly-immuno
c	37	16.2	77.1	3857	21	Z94129	Haematopoietic ste
c	38	16	76.2	2007	13	Q27287	DNA encoding TAP.
	39	16	76.2	7686	21	Z29335	Human acrosome rea
	40	15.8	75.2	775	21	F14522	Aspergillus oryzae
c	41	15.4	73.3	784	21	F11868	Aspergillus oryzae
c	42	15.4	73.3	5278	18	V04446	Rat programmed cel
	43	15.2	72.4	251	19	X12564	Human biallelic po
c	44	15.2	72.4	300	20	Z14540	Human gene express
c	45	15.2	72.4	485	21	A15088	Gene fragment homo

ALIGNMENTS

RESULT 1
T76118
ID T76118 standard; DNA; 21 BP.
XX
AC T76118;
XX
DT 12-SEP-1997 (first entry)
XX
DE Human eosinophil cationic protein antisense oligonucleotide HSECPAS1.
XX
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; ss.
XX
OS Synthetic.
XX
PN WO9640162-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09306.
XX
PR 07-JUN-1995; 95US-0474497.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Metzger WJ, Nyce JW;
XX
DR WPI; 1997-051871/05.
XX
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject
XX
PS Claim 5; Page 26; 71pp; English.

```
XX
CC   A method for treating airway disease in a subject has been produced,
CC   which involves the topical administration of an essentially adenosine
CC   free antisense oligonucleotide (ON) to the airway epithelium of the
CC   subject. The present sequence is an antisense oligonucleotide
CC   HSECPAS1 specific for the human eosinophil cationic protein. The method
CC   can be used to treat airway diseases such as cystic fibrosis, asthma,
CC   chronic obstructive pulmonary disease, bronchitis and other
CC   airway diseases characterised by an inflammatory response. By
CC   eliminating adenosine from the antisense ON, its liberation upon
CC   antisense degradation is prevented, thereby preventing adenosine-
CC   induced bronchoconstriction in patients with hyper-reactive airways.
XX
SQ   Sequence 21 BP; 0 A; 9 C; 4 G; 8 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 18;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db      1 cctccttcctggtctgtctgc 21


RESULT   2
X54596
ID   X54596 standard; DNA; 81 BP.
XX
AC   X54596;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Eosinophil cationic protein antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 46; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (X52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences X55272-74. These multiple target
CC   oligonucleotides (specifically X55180-271) can be used for the antisense
CC   treatment of diseases and conditions. Typical diseases and conditions
CC   are those associated with impaired respiration and inflammation,
CC   including lung diseases, pulmonary vasoconstriction, inflammation,
CC   allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC   respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC   hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC   carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC   cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC   metastases, as well as all types of cancers which may metastasize or have
CC   metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 81 BP; 0 A; 21 C; 20 G; 25 T; 15 other;


  Query Match             100.0%;  Score 21;  DB 20;  Length 81;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db      1 cctccttcctggtctgtctgc 21


RESULT   3
F20165
ID   F20165 standard; DNA; 81 BP.
XX
AC   F20165;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human eosinophil cationic protein polynucleotide fragment #1732.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Claim 14; Page 142; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
```

CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 81 BP; 0 A; 21 C; 20 G; 25 T; 15 other;

Query Match 100.0%; Score 21; DB 21; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCCTTCCTGGTCTGTCTGC 21
||||||||||||||||||||
Db 1 cctccttcctggtctgtctgc 21

RESULT 4
A34043
ID A34043 standard; DNA; 81 BP.
XX
AC A34043;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:1732.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 480; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
SQ Sequence 81 BP; 0 A; 21 C; 20 G; 25 T; 15 other;

Query Match 100.0%; Score 21; DB 21; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCCTTCCTGGTCTGTCTGC 21
||||||||||||||||||||
Db 1 cctccttcctggtctgtctgc 21

RESULT 5
F21294/c
ID F21294 standard; DNA; 715 BP.
XX
AC F21294;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2861.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX

PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 1288; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 715 BP; 185 A; 199 C; 141 G; 190 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 715;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCCTTCCTGGTCTGTCTGC 21
||||||||||||||||||||
Db 450 CCTCCTTCCTGGTCTGTCTGC 430

RESULT 6
A35172/c
ID A35172 standard; DNA; 715 BP.
XX
AC A35172;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:46.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 1205; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
SQ Sequence 715 BP; 185 A; 199 C; 141 G; 190 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 715;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCCTTCCTGGTCTGTCTGC 21
||||||||||||||||||||
Db 450 CCTCCTTCCTGGTCTGTCTGC 430

RESULT 7
F21293/c
ID F21293 standard; DNA; 718 BP.
XX
AC F21293;

XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2860.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 1288; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 718 BP; 187 A; 197 C; 144 G; 190 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 718;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCCTTCCTGGTCTGTCTGC 21
||||||||||||||||||||
Db 448 CCTCCTTCCTGGTCTGTCTGC 428

RESULT 8
A35171/c
ID A35171 standard; DNA; 718 BP.
XX
AC A35171;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:45.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 1205; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not

```
CC   match up with their corresponding SEQ ID NO: sequences given in the
CC   sequence listing.
XX
SQ   Sequence 718 BP; 187 A; 197 C; 144 G; 190 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 21;  Length 718;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    448 CCTCCTTCCTGGTCTGTCTGC 428


RESULT   9
F21295/c
ID   F21295 standard; DNA; 1452 BP.
XX
AC   F21295;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human low adenosine antisense oligonucleotide related sequence #2862.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Disclosure; Page 1288-1289; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC   and antisense oligonucleotides used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 1452 BP; 380 A; 376 C; 323 G; 373 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 21;  Length 1452;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    951 CCTCCTTCCTGGTCTGTCTGC 931


RESULT  10
A35173/c
ID   A35173 standard; DNA; 1452 BP.
XX
AC   A35173;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide 2nd SEQ ID NO:47.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
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PD   24-FEB-2000.
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PF   03-AUG-1999;   99WO-US17712.
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PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
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DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Disclosure; Page 1205-1206; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
```

```
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. A32313 to A35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC   to A33992) are specifically claimed ONs from the present invention.
CC   N.B. Sequences given in the disclosure of the present invention do not
CC   match up with their corresponding SEQ ID NO: sequences given in the
CC   sequence listing.
XX
SQ   Sequence 1452 BP; 380 A; 376 C; 323 G; 373 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 21;  Length 1452;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTGC 21
           |||||||||||||||||||||
Db     951 CCTCCTTCCTGGTCTGTCTGC 931


RESULT  11
F21296/c
ID   F21296 standard; DNA; 2885 BP.
XX
AC   F21296;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human low adenosine antisense oligonucleotide related sequence #2863.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Disclosure; Page 1289; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC   and antisense oligonucleotides used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 2885 BP; 752 A; 772 C; 608 G; 753 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 21;  Length 2885;
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Qy       1 CCTCCTTCCTGGTCTGTCTGC 21
           |||||||||||||||||||||
Db    2384 CCTCCTTCCTGGTCTGTCTGC 2364


RESULT  12
A35174/c
ID   A35174 standard; DNA; 2885 BP.
XX
AC   A35174;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide 2nd SEQ ID NO:48.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
```

PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 1206; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
SQ Sequence 2885 BP; 752 A; 772 C; 608 G; 753 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 2885;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCCTTCCTGGTCTGTCTGC 21
||||||||||||||||||||
Db 2384 CCTCCTTCCTGGTCTGTCTGC 2364

RESULT 13
F20844
ID F20844 standard; DNA; 7033 BP.
XX
AC F20844;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide #2411.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Claim 14; Page 637-639; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 7033 BP; 82 A; 2193 C; 2184 G; 2057 T; 517 other;

Query Match 100.0%; Score 21; DB 21; Length 7033;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCCTTCCTGGTCTGTCTGC 21
||||||||||||||||||||
Db 1 cctccttcctggtctgtctgc 21

RESULT 14
A34722
ID A34722 standard; DNA; 7033 BP.
XX
AC A34722;

```
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2411.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Disclosure; Page 569-571; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. A32313 to A35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC   to A33992) are specifically claimed ONs from the present invention.
CC   N.B. Sequences given in the disclosure of the present invention do not
CC   match up with their corresponding SEQ ID NO: sequences given in the
CC   sequence listing.
XX
SQ   Sequence 7033 BP; 82 A; 2193 C; 2184 G; 2057 T; 517 other;


  Query Match           100.0%;  Score 21;  DB 21;  Length 7033;
  Best Local Similarity  100.0%;  Pred. No. 1.7;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db      1 cctccttcctggtctgtctgc 21
```

```
RESULT  15
X55274
ID   X55274 standard; DNA; 7036 BP.
XX
AC   X55274;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Human factor-related antisense polynucleotide.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 25-27; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (X52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences X55272-74. These multiple target
CC   oligonucleotides (specifically X55180-271) can be used for the antisense
CC   treatment of diseases and conditions. Typical diseases and conditions
CC   are those associated with impaired respiration and inflammation,
CC   including lung diseases, pulmonary vasoconstriction, inflammation,
CC   allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC   respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC   hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC   carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC   cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC   metastases, as well as all types of cancers which may metastasize or have
CC   metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 7036 BP; 82 A; 2194 C; 2185 G; 2058 T; 517 other;


  Query Match           100.0%;  Score 21;  DB 20;  Length 7036;
  Best Local Similarity  100.0%;  Pred. No. 1.7;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db      1 cctccttcctggtctgtctgc 21
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Search completed: April 20, 2001, 00:12:59
Job time: 10021 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:24:57 ; Search time 7150.85 Seconds
(without alignments)
0.429 Million cell updates/sec

Title: US-09-016-464-18
Perfect score: 21
Sequence: 1 CCTCCTTCCTGGTCTGTCTGC 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	21	100.0	285	172	BG014139	BG014139 IL5-GN023
c 3	21	100.0	302	170	BF902198	BF902198 IL5-MT020
4	21	100.0	323	9	AA587166	AA587166 nn74c10.s
5	21	100.0	597	110	AW075940	AW075940 xa82a02.x
c 6	19	90.5	1569	150	BF570099	BF570099 602185939
c 7	18.4	87.6	96	11	AA716588	AA716588 zg66d04.s
c 8	18.4	87.6	137	215	AZ071781	AZ071781 RPCI-23-4
9	18.4	87.6	273	115	AW468752	AW468752 hd27e07.x
10	18.4	87.6	482	148	BF441931	BF441931 258400 MA
11	18.4	87.6	492	207	AQ482290	AQ482290 RPCI-11-2
12	18.4	87.6	618	204	AQ315451	AQ315451 RPCI11-10
13	18.4	87.6	1002	231	CNS03LBT	AL249266 Tetraodon
c 14	17.8	84.8	220	173	BG092228	BG092228 mac06f10.
c 15	17.8	84.8	222	9	AA562957	AA562957 v157c06.r
c 16	17.8	84.8	230	120	AW812057	AW812057 RC5-ST017
17	17.8	84.8	237	173	BG090438	BG090438 mac06f10.
18	17.8	84.8	268	121	AW878939	AW878939 MR1-OT001

	19	17.8	84.8	275	163	BE133367	BE133367 ug32c07.y
	20	17.8	84.8	277	148	BF455872	BF455872 UI-M-BZ1-
	21	17.8	84.8	295	3	AA172447	AA172447 mt03d11.r
	22	17.8	84.8	303	226	AZ698812	AZ698812 RPCI-23-2
c	23	17.8	84.8	337	138	BE692014	BE692014 uv70d01.x
c	24	17.8	84.8	367	117	AW551216	AW551216 L0075D08-
	25	17.8	84.8	383	137	BE634214	BE634214 uv70d01.y
	26	17.8	84.8	401	4	AA221880	AA221880 mv52h05.r
c	27	17.8	84.8	401	146	BF329952	BF329952 PM4-BN029
c	28	17.8	84.8	407	138	BE690759	BE690759 uw58g04.x
	29	17.8	84.8	419	13	AA870628	AA870628 vq24a12.r
	30	17.8	84.8	429	3	AA184116	AA184116 mt22f04.r
	31	17.8	84.8	447	3	AA175320	AA175320 ms86b07.r
c	32	17.8	84.8	448	142	BE990692	BE990692 UI-M-BZ1-
	33	17.8	84.8	449	12	AA832759	AA832759 vw46a10.r
c	34	17.8	84.8	462	10	AA700071	AA700071 zi62e04.s
c	35	17.8	84.8	463	175	C77473	C77473 C77473 Mous
	36	17.8	84.8	470	4	AA273661	AA273661 vb92e12.r
	37	17.8	84.8	480	122	AW990166	AW990166 uf34h04.y
c	38	17.8	84.8	483	172	BG065930	BG065930 H3037A03-
	39	17.8	84.8	488	14	AI006694	AI006694 ua67e04.r
	40	17.8	84.8	502	173	BG079197	BG079197 H3037A03-
c	41	17.8	84.8	519	140	BE853286	BE853286 uw87d05.x
c	42	17.8	84.8	545	138	BE688759	BE688759 uw49f05.x
	43	17.8	84.8	690	166	BE375439	BE375439 601225610
	44	17.8	84.8	796	141	BE916162	BE916162 601666783
c	45	17.4	82.9	298	125	BB130738	BB130738 BB130738

ALIGNMENTS

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RESULT   1
BF895434/c
LOCUS       BF895434      231 bp    mRNA            EST       18-JAN-2001
DEFINITION  CM0-MT0151-211100-690-g08 MT0151 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF895434
VERSION     BF895434.1  GI:12286893
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 231)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM0&t2=CM0-MT0151-
            211100-690-g08&t3=2000-11-21&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 14
            High quality sequence stop: 231.
FEATURES             Location/Qualifiers
     source          1. .231
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="MT0151"
                     /dev_stage="Adult"
                     /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT       62 a     60 c     49 g     60 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 170;  Length 231;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTGC 21
           |||||||||||||||||||||
Db     129 CCTCCTTCCTGGTCTGTCTGC 109


RESULT   2
BG014139
LOCUS       BG014139      285 bp    mRNA            EST       24-JAN-2001
DEFINITION  IL5-GN0238-201200-362-c05 GN0238 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG014139
VERSION     BG014139.1  GI:12465039
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL5&t2=IL5-GN0238-
            201200-362-c05&t3=2000-12-20&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 285.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="GN0238"
                     /dev_stage="Adult"
                     /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
                     ; Site_2: SmaI; A mini-library was made by cloning
                     products derived from  ORESTES PCR (U.S. Letters Patent
                     application No. 196,716 -  Ludwig Institute for Cancer
                     Research) profiles into  the pUC 18 vector. Reverse
                     transcription of tissue mRNA and cDNA amplification were
                     performed under low stringency conditions."
BASE COUNT       77 a     55 c     68 g     85 t
ORIGIN
```

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  Query Match             100.0%;  Score 21;  DB 172;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db     12 CCTCCTTCCTGGTCTGTCTGC 32


RESULT   3
BF902198/c
LOCUS       BF902198      302 bp    mRNA            EST       18-JAN-2001
DEFINITION  IL5-MT0207-121200-339-e11 MT0207 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF902198
VERSION     BF902198.1  GI:12293657
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 302)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-MT0207-
            121200-339-e11&t3=2000-12-12&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 301.
FEATURES             Location/Qualifiers
     source          1. .302
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="MT0207"
                     /dev_stage="Adult"
                     /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT       91 a     71 c     60 g     80 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 170;  Length 302;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    274 CCTCCTTCCTGGTCTGTCTGC 254


RESULT   4
AA587166
LOCUS       AA587166      323 bp    mRNA            EST       26-SEP-1997
DEFINITION  nn74c10.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1089618 3'
            similar to gb:X55990_rna1 EOSINOPHIL CATIONIC PROTEIN PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   AA587166
VERSION     AA587166.1  GI:2397980
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 323)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Stratagene, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llni.gov/bbrp/image/image.html
            Insert Length: 439   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .323
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1089618"
                     /clone_lib="NCI_CGAP_Lar1"
                     /tissue_type="larynx"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: larynx; Vector: Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. Larynx. 5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'
                     Average insert size:  0.9 kb."
BASE COUNT       84 a     59 c     96 g     84 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 9;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    266 CCTCCTTCCTGGTCTGTCTGC 286


RESULT   5
AW075940
LOCUS       AW075940      597 bp    mRNA            EST       13-OCT-1999
DEFINITION  xa82a02.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573258 3'
            similar to gb:X55990_rna1 EOSINOPHIL CATIONIC PROTEIN PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   AW075940
VERSION     AW075940.1  GI:6030938
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 597)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
```

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            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,
            Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .597
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2573258"
                     /clone_lib="NCI_CGAP_CML1"
                     /tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL
                     rearrangement positive, includes both chronic phase and
                     myeloid blast crisis"
                     /lab_host="DH10B"
                     /note="Organ: whole blood; Vector: pCMV-SPORT6; Site_1:
                     SalI; Site_2: NotI; Cloned unidirectionally.  Primer:
                     Oligo dT.   Library constructed by Life Technologies."
BASE COUNT      157 a    111 c    174 g    155 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 110;  Length 597;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    267 CCTCCTTCCTGGTCTGTCTGC 287


RESULT   6
BF570099/c
LOCUS       BF570099     1569 bp    mRNA            EST       12-DEC-2000
DEFINITION  602185939T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310576 3',
            mRNA sequence.
ACCESSION   BF570099
VERSION     BF570099.1  GI:11643811
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1569)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Linehan
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1185  row: m  column: 09
            High quality sequence start: 10
            High quality sequence stop: 642.
FEATURES             Location/Qualifiers
     source          1. .1569
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4310576"
                     /clone_lib="NIH_MGC_45"
                     /tissue_type="renal carcinoma (ascites)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life  Technologies). Note: this is a
                     NIH_MGC Library. |"
BASE COUNT      584 a    375 c    399 g    211 t
ORIGIN


  Query Match             90.5%;  Score 19;  DB 150;  Length 1569;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 CTCCTTCCTGGTCTGTCTG 20
          |||||||||||||||||||
Db   1546 CTCCTTCCTGGTCTGTCTG 1528


RESULT   7
AA716588/c
LOCUS       AA716588       96 bp    mRNA            EST       29-DEC-1997
DEFINITION  zg66d04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
            IMAGE:398311 3' similar to gb:J04794 ALCOHOL DEHYDROGENASE (HUMAN
            );; mRNA sequence.
ACCESSION   AA716588
VERSION     AA716588.1  GI:2728862
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 96)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .96
                     /organism="Homo sapiens"
                     /db_xref="GDB:1306134"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:398311"
                     /clone_lib="Soares_fetal_heart_NbHH19W"
                     /sex="unknown"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
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                the Not I and Eco RI sites of a modified pT7T3 vector
                (Pharmacia). Library went through one round of
                normalization to a Cot = 5. Library constructed by
                M.Fatima Bonaldo. This library was constructed from the
                same fetus as the fetal lung library, Soares fetal lung
                NbHL19W."
BASE COUNT       33 a     20 c     24 g     19 t
ORIGIN


  Query Match             87.6%;  Score 18.4;  DB 11;  Length 96;
  Best Local Similarity   95.0%;  Pred. No. 3.6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CTCCTTCCTGGTCTGTCTGC 21
          |||||||| ||||||||||
Db     76 CTCCTTCCTAGTCTGTCTGC 57


RESULT   8
AZ071781/c
LOCUS       AZ071781      137 bp    DNA             GSS       31-MAR-2000
DEFINITION  RPCI-23-435M13.TV RPCI-23 Mus musculus genomic clone RPCI-23-435M13
            , DNA sequence.
ACCESSION   AZ071781
VERSION     AZ071781.1  GI:7364678
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 137)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
            ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-435M13.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 435  row: M  column: 13
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .137
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-435M13"
                     /clone_lib="RPCI-23"
                     /sex="Female"
                     /lab_host="DH10B"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and  partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI  sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies).   "
BASE COUNT       48 a     55 c     34 g      0 t
ORIGIN


  Query Match             87.6%;  Score 18.4;  DB 215;  Length 137;
  Best Local Similarity   95.0%;  Pred. No. 3.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTG 20
          |||||||||||| |||||||
Db     36 CCTCCTTCCTGGCCTGTCTG 17


RESULT   9
AW468752
LOCUS       AW468752      273 bp    mRNA            EST       24-FEB-2000
DEFINITION  hd27e07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:2910756 3', mRNA sequence.
ACCESSION   AW468752
VERSION     AW468752.1  GI:7038858
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 273)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .273
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2910756"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo.  "
BASE COUNT       55 a     64 c     61 g     93 t
ORIGIN


  Query Match             87.6%;  Score 18.4;  DB 115;  Length 273;
  Best Local Similarity   95.0%;  Pred. No. 4.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CTCCTTCCTGGTCTGTCTGC 21
          |||||||||||| ||||||||
Db    141 CTCCTTCCTGGGCTGTCTGC 160


RESULT  10
BF441931
LOCUS       BF441931      482 bp    mRNA            EST       01-DEC-2000
DEFINITION  258400 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BF441931
VERSION     BF441931.1  GI:11502023
KEYWORDS    EST.
SOURCE      pig.
```

```
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 482)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 87  row: M  column: 18
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .482
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 2PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT       83 a    145 c    143 g    111 t
ORIGIN


  Query Match             87.6%;  Score 18.4;  DB 148;  Length 482;
  Best Local Similarity   95.0%;  Pred. No. 4.4e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTG 20
           | ||||||||||||||||||
Db      14 CGTCCTTCCTGGTCTGTCTG 33


RESULT  11
AQ482290
LOCUS       AQ482290      492 bp    DNA             GSS       24-APR-1999
DEFINITION  RPCI-11-257P22.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-257P22
            , DNA sequence.
ACCESSION   AQ482290
VERSION     AQ482290.1  GI:4669694
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 492)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
            ,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: RPCI-11-257P22.TV
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .492
                     /organism="Homo sapiens"
                     /db_xref="GDB:7598685"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-257P22"
                     /clone_lib="RPCI-11"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
BASE COUNT      144 a     94 c    104 g    150 t
ORIGIN


  Query Match             87.6%;  Score 18.4;  DB 207;  Length 492;
  Best Local Similarity   95.0%;  Pred. No. 4.4e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CTCCTTCCTGGTCTGTCTGC 21
           |||||||||||||||| ||||
Db     265 CTCCTTCCTGGTCTGCCTGC 284


RESULT  12
AQ315451
LOCUS       AQ315451      618 bp    DNA             GSS       04-MAY-1999
DEFINITION  RPCI11-104A3.TV RPCI-11 Homo sapiens genomic clone RPCI-11-104A3,
            DNA sequence.
ACCESSION   AQ315451
VERSION     AQ315451.1  GI:4046914
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 618)
  AUTHORS   Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
            Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
  TITLE     Use of human BAC End Sequences for Sequence-Ready Map Building
  JOURNAL   Unpublished (1998)
COMMENT     Other_GSSs: RPCI11-104A3.TJ
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genetics (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .618
                     /organism="Homo sapiens"
                     /db_xref="GDB:7539554"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-104A3"
                     /clone_lib="RPCI-11"
                     /sex="Male"
```

```
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
BASE COUNT       126 a    163 c    173 g    156 t
ORIGIN


  Query Match             87.6%;  Score 18.4;  DB 204;  Length 618;
  Best Local Similarity   95.0%;  Pred. No. 4.6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CTCCTTCCTGGTCTGTCTGC 21
           || ||||||||||||||||
Db       9 CTGCTTCCTGGTCTGTCTGC 28


RESULT  13
CNS03LBT
LOCUS       CNS03LBT     1002 bp    DNA             GSS       17-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            035I24 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL249266
VERSION     AL249266.1  GI:7970278
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
            Holacanthopterygii; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 1002)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1002)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1002)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1002
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="035I24"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG035BE12SP1-end :
                     PUC-Ori"
BASE COUNT       228 a    273 c    253 g    243 t      5 others
ORIGIN


  Query Match             87.6%;  Score 18.4;  DB 231;  Length 1002;
  Best Local Similarity   95.0%;  Pred. No. 4.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTG 20
           |||||||||||||||||  ||
Db     614 CCTCCTTCCTGGTCTGTGTG 633


RESULT  14
BG092228/c
LOCUS       BG092228      220 bp    mRNA            EST       26-JAN-2001
DEFINITION  mac06f10.x1 Soares mouse 3NbMS Mus musculus cDNA clone
            IMAGE:3999115 3', mRNA sequence.
ACCESSION   BG092228
VERSION     BG092228.1  GI:12574780
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 220)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Other_ESTs: mac06f10.y1
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1496843.
FEATURES             Location/Qualifiers
     source          1. .220
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3999115"
                     /clone_lib="Soares mouse 3NbMS"
                     /sex="male"
                     /tissue_type="Spleen"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTGTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through
                     three rounds of normalization, and was constructed by
                     Bento Soares and M.Fatima Bonaldo."
BASE COUNT        80 a     44 c     41 g     55 t
ORIGIN


  Query Match             84.8%;  Score 17.8;  DB 173;  Length 220;
  Best Local Similarity   90.5%;  Pred. No. 7.4e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTGC 21
           ||||||  |||| |||||||||
Db     160 CCTCCTACCTGTTCTGTCTGC 140


RESULT  15
AA562957/c
LOCUS       AA562957      222 bp    mRNA            EST       18-AUG-1997
DEFINITION  v157c06.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
            IMAGE:976330 5', mRNA sequence.
ACCESSION   AA562957
VERSION     AA562957.1  GI:2334422
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 222)
```

```
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:557058
            Seq primer: -28m13 rev1 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .222
                     /organism="Mus musculus"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:976330"
                     /clone_lib="Stratagene mouse skin (#937313)"
                     /sex="females"
                     /tissue_type="whole skin"
                     /dev_stage="11 weeks old"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
                     ; Site_2: XhoI; Cloned unidirectionally.  Primer: Oligo
                     dT. Whole skin from 11 week old C57BL/6 female mice.
                     Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
                     adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor
                     sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT       84 a     43 c     43 g     52 t
ORIGIN


  Query Match             84.8%;  Score 17.8;  DB 9;  Length 222;
  Best Local Similarity   90.5%;  Pred. No. 7.4e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTGC 21
           |||||| |||| |||||||||
Db     174 CCTCCTACCTGTTCTGTCTGC 154



Search completed: April 19, 2001, 23:25:00
Job time: 8177 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:03:44 ; Search time 280.46 Seconds
(without alignments)
13.074 Million cell updates/sec

Title: US-09-016-464-18
Perfect score: 21
Sequence: 1 CCTCCTTCCTGGTCTGTCTGC 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	16.2	77.1	3517	2	US-08-642-406A-20	Sequence 20, Appl
c	2	16.2	77.1	3517	3	US-08-434-000A-1	Sequence 1, Appli
c	3	15.2	72.4	591	3	US-08-545-809A-17	Sequence 17, Appl
	4	15.2	72.4	868	2	US-08-993-228-15	Sequence 15, Appl
	5	15.2	72.4	1269	1	US-08-396-218-1	Sequence 1, Appli
	6	15.2	72.4	1269	1	US-08-760-116-1	Sequence 1, Appli
	7	15.2	72.4	2842	1	US-08-175-388-3	Sequence 3, Appli
	8	15.2	72.4	2842	2	US-08-779-620-3	Sequence 3, Appli
	9	15.2	72.4	2842	2	US-08-818-726-3	Sequence 3, Appli
c	10	15.2	72.4	12311	4	US-08-750-717-1	Sequence 1, Appli
c	11	14.8	70.5	1574	3	US-08-845-546-1	Sequence 1, Appli
	12	14.8	70.5	1736	1	US-08-518-474-7	Sequence 7, Appli
	13	14.8	70.5	3266	1	US-08-369-043-3	Sequence 3, Appli
	14	14.6	69.5	41	2	US-08-343-443B-24	Sequence 24, Appl
c	15	14.6	69.5	648	1	US-08-681-812-1	Sequence 1, Appli
	16	14.6	69.5	658	4	US-08-792-013-5	Sequence 5, Appli
c	17	14.6	69.5	1250	1	US-08-331-657-5	Sequence 5, Appli
c	18	14.6	69.5	1894	3	US-07-728-220C-1	Sequence 1, Appli
c	19	14.6	69.5	1953	3	US-08-826-246-1	Sequence 1, Appli
c	20	14.6	69.5	1953	3	US-08-944-495-1	Sequence 1, Appli
c	21	14.6	69.5	1953	3	US-09-126-640-1	Sequence 1, Appli
c	22	14.6	69.5	3066	1	US-08-142-439A-1	Sequence 1, Appli
c	23	14.6	69.5	3066	2	US-08-869-477-1	Sequence 1, Appli
c	24	14.6	69.5	3403	4	US-08-448-489-2	Sequence 2, Appli
c	25	14.6	69.5	3437	4	US-08-704-711A-9	Sequence 9, Appli
c	26	14.6	69.5	3456	4	US-08-704-711A-8	Sequence 8, Appli
	27	14.6	69.5	3777	3	US-09-121-321-15	Sequence 15, Appl
	28	14.6	69.5	3907	4	US-08-475-742-1	Sequence 1, Appli
	29	14.6	69.5	4406	1	US-08-369-043-1	Sequence 1, Appli
c	30	14.6	69.5	87350	3	US-08-781-891-79	Sequence 79, Appl
c	31	14.4	68.6	297	3	US-08-894-699-3	Sequence 3, Appli
c	32	14.4	68.6	358	2	US-08-713-052-1	Sequence 1, Appli
	33	14.4	68.6	1371	2	US-08-428-713-1	Sequence 1, Appli
	34	14.4	68.6	1371	3	US-08-904-179-1	Sequence 1, Appli
	35	14.4	68.6	1374	2	US-08-428-713-9	Sequence 9, Appli
	36	14.4	68.6	1374	3	US-08-904-179-9	Sequence 9, Appli
c	37	14.4	68.6	2474	2	US-08-666-392A-2	Sequence 2, Appli
c	38	14.4	68.6	2550	6	5258287-23	Patent No. 5258287
	39	14.4	68.6	4157	2	US-08-162-146-2	Sequence 2, Appli
	40	14.2	67.6	109	4	US-08-961-810-38	Sequence 38, Appl
	41	14.2	67.6	109	4	US-08-352-902D-38	Sequence 38, Appl
c	42	14.2	67.6	152	1	US-08-136-277-15	Sequence 15, Appl
c	43	14.2	67.6	152	2	US-08-479-403-15	Sequence 15, Appl
c	44	14.2	67.6	152	3	US-08-835-734-15	Sequence 15, Appl
	45	14.2	67.6	377	4	US-08-961-810-19	Sequence 19, Appl

ALIGNMENTS

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RESULT 1
US-08-642-406A-20/c
; Sequence 20, Application US/08642406A
; Patent No. 5959177
;  GENERAL INFORMATION:
;    APPLICANT:  Hein, Mich B.
;    APPLICANT:  Hiatt, Andrew C.
;    APPLICANT:  Ma, Julian K.C.
;    TITLE OF INVENTION:  TRANSGENIC PLANTS EXPRESSING ASSEMBLED
;    TITLE OF INVENTION:  SECRETORY ANTIBODIES
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  THE SCRIPPS RESEARCH INSTITUTE
;      STREET:  10666 No. 5959177th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/642,406A
;      FILING DATE:  03-MAY-1996
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/591,823
;      FILING DATE:  02-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/427,765
;      FILING DATE:  27-OCT-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Logan, April C.
;      REGISTRATION NUMBER:  33,950
;      REFERENCE/DOCKET NUMBER:  184.2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-642-406A-20
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  Query Match             77.1%;  Score 16.2;  DB 2;  Length 3517;
  Best Local Similarity   85.7%;  Pred. No. 61;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          || |||  ||||||||||||
Db   2770 CCCCCTCTCTGGTCTGTCTGC 2750


RESULT   2
US-08-434-000A-1/c
; Sequence 1, Application US/08434000A
; Patent No. 6046037
;  GENERAL INFORMATION:
;    APPLICANT:  ANDREW C. HIATT, JULIAN
;    APPLICANT:  K.-C. MA, THOMAS LEHNER
;    TITLE OF INVENTION:  IMMUNOGLOBULINS CONTAINING PROTECTION
;    TITLE OF INVENTION:  PROTEINS IN PLANTS AND THEIR USES
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/434,000A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:          1
;      APPLICATION NUMBER:  08/367,395
;      FILING DATE:  12/30/94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Guise, Jeffrey W.
;      REGISTRATION NUMBER:  34,613
;      REFERENCE/DOCKET NUMBER:  212/127
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 552-8400
;      TELEFAX:  (619) 552-0159
;      TELEX:  67-3510
;      TELEX:  SEQUENCE LISTING
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      TOPOLOGY:  DESCRIPTION:    Rabbit polyimmunoglobulin receptor
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  124....2445
US-08-434-000A-1


  Query Match             77.1%;  Score 16.2;  DB 3;  Length 3517;
  Best Local Similarity   85.7%;  Pred. No. 61;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          || |||  ||||||||||||
Db   2770 CCCCCTCTCTGGTCTGTCTGC 2750


RESULT   3
US-08-545-809A-17/c
; Sequence 17, Application US/08545809A
; Patent No. 6096878
;  GENERAL INFORMATION:
;    APPLICANT:  Honjo, Tasuku
;    APPLICANT:  Matsuda, Fumihiko
;    TITLE OF INVENTION:  HUMAN IMMUNOGLOBULIN VH GENE
;    TITLE OF INVENTION:  SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;    NUMBER OF SEQUENCES:  145
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/545,809A
;      FILING DATE:  27-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP93/00603
;      FILING DATE:  10-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  06501/004001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  591 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  human lymphoblast
;      CELL LINE:  CGM1
US-08-545-809A-17


  Query Match             72.4%;  Score 15.2;  DB 3;  Length 591;
  Best Local Similarity   85.0%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTG 20
          ||||||||||||  | ||||
Db    533 CCTCCTTCCTGGGGTTTCTG 514


RESULT   4
US-08-993-228-15
; Sequence 15, Application US/08993228
; Patent No. 5976838
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John M.
;    APPLICANT:  LaVallie, Edward R.
;    APPLICANT:  Racie, Lisa A.
;    APPLICANT:  Merberg, David
;    APPLICANT:  Treacy, Maurice
;    APPLICANT:  Spaulding, Vikki
```

```
;    APPLICANT:  Agostino, Michael J.
;    TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES
;    TITLE OF INVENTION:  ENCODING THEM
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/993,228
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sprunger, Suzanne A.
;      REGISTRATION NUMBER:  41,323
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8284
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  868 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-993-228-15


  Query Match             72.4%;  Score 15.2;  DB 2;  Length 868;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTG 20
          |||||| |||| |||| |||
Db    702 CCTCCTCCCTGTTCTGGCTG 721


RESULT   5
US-08-396-218-1
; Sequence 1, Application US/08396218
; Patent No. 5695966
;  GENERAL INFORMATION:
;    APPLICANT:  INVENTI, Augusto
;    APPLICANT:  BREME, Umberto
;    APPLICANT:  COLOMBO, Anna L
;    APPLICANT:  HUTCHINSON, Charles R
;    APPLICANT:  OTTEN, Sharee
;    APPLICANT:  SCOTTI, Claudio
;    TITLE OF INVENTION:  PROCESS FOR PREPARING DOXORUBICIN
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIKAIDO, MARMELSTEIN, MURRAY & ORAM
;      STREET:  655 Fifteenth Street, N. W., Suite 330 - G
;      STREET:  Street Lobby
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/396,218
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KITTS, Monica C
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P1615-5002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/638-5000
;      TELEFAX:  202/638-4810
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1269 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Streptomyces peucetius
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1269
US-08-396-218-1


  Query Match             72.4%;  Score 15.2;  DB 1;  Length 1269;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 CTCCTTCCTGGTCTGTCTGC 21
          |||||||||| ||  ||||
Db    801 CTCCTTCCTGGGCTTCCTGC 820


RESULT   6
US-08-760-116-1
; Sequence 1, Application US/08760116
; Patent No. 5786190
;  GENERAL INFORMATION:
;    APPLICANT:  INVENTI, Augusto
;    APPLICANT:  BREME, Umberto
;    APPLICANT:  COLOMBO, Anna L
;    APPLICANT:  HUTCHINSON, Charles R
;    APPLICANT:  OTTEN, Sharee
;    APPLICANT:  SCOTTI, Claudio
;    TITLE OF INVENTION:  PROCESS FOR PREPARING DOXORUBICIN
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
;      STREET:  655 Fifteenth Street, N. W., Suite 330 - G
;      STREET:  Street Lobby
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/760,116
;      FILING DATE:  3-DEC-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/396,218
;      FILING DATE:  27-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KITTS, Monica C
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P1615-6007
;    TELECOMMUNICATION INFORMATION:
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;       TELEPHONE:  202/638-5000
;       TELEFAX:  202/638-4810
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1269 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Streptomyces peucetius
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1269
US-08-760-116-1


  Query Match             72.4%;  Score 15.2;  DB 1;  Length 1269;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 CTCCTTCCTGGTCTGTCTGC 21
           |||||||||||  ||  ||||
Db     801 CTCCTTCCTGGGCTTCCTGC 820


RESULT   7
US-08-175-388-3
; Sequence 3, Application US/08175388
; Patent No. 5641674
;  GENERAL INFORMATION:
;    APPLICANT:  DEHOUX, PIERRE
;    APPLICANT:  DAVIES, JULIAN
;    TITLE OF INVENTION:  Nucleotide Sequences and Proteins
;    TITLE OF INVENTION:  Conferring Cycloheximide Resistance
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/175,388
;      FILING DATE:  09-JUN-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/FR92/00685
;      FILING DATE:  15-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 9108906
;      FILING DATE:  15-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5641674man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  660-071-0 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2842 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-175-388-3


  Query Match             72.4%;  Score 15.2;  DB 1;  Length 2842;
  Best Local Similarity   85.0%;  Pred. No. 1.6e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTG 20
           ||| | ||||||||| |||||
Db     259 CCTTCCTCCTGGTCGGTCTG 278


RESULT   8
US-08-779-620-3
; Sequence 3, Application US/08779620
; Patent No. 5830997
;  GENERAL INFORMATION:
;    APPLICANT:  DEHOUX, PIERRE
;    APPLICANT:  DAVIES, JULIAN
;    TITLE OF INVENTION:  Nucleotide Sequences and Proteins
;    TITLE OF INVENTION:  Conferring Cycloheximide Resistance
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/779,620
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,388
;      FILING DATE:  09-JUN-1994
;      APPLICATION NUMBER:  PCT/FR92/00685
;      FILING DATE:  15-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 9108906
;      FILING DATE:  15-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5830997man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  660-071-0 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2842 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-779-620-3


  Query Match             72.4%;  Score 15.2;  DB 2;  Length 2842;
  Best Local Similarity   85.0%;  Pred. No. 1.6e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTG 20
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          ||| | |||||||| |||||
Db    259 CCTTCCTCCTGGTCGGTCTG 278


RESULT   9
US-08-818-726-3
; Sequence 3, Application US/08818726
; Patent No. 5958687
;  GENERAL INFORMATION:
;    APPLICANT:  DEHOUX, PIERRE
;    APPLICANT:  DAVIES, JULIAN
;    TITLE OF INVENTION:  Nucleotide Sequences and Proteins
;    TITLE OF INVENTION:  Conferring Cycloheximide Resistance
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/818,726
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,388
;      FILING DATE:  09-JUN-1994
;      APPLICATION NUMBER:  PCT/FR92/00685
;      FILING DATE:  15-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 9108906
;      FILING DATE:  15-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5958687man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  660-071-0 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2842 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-818-726-3


  Query Match             72.4%;  Score 15.2;  DB 2;  Length 2842;
  Best Local Similarity   85.0%;  Pred. No. 1.6e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTG 20
          ||| | |||||||| |||||
Db    259 CCTTCCTCCTGGTCGGTCTG 278


RESULT  10
US-08-750-717-1/c
; Sequence 1, Application US/08750717
; Patent No. 6180109
;  GENERAL INFORMATION:
;    APPLICANT:  MOORMANN, Robertus J. M.
;    APPLICANT:  VAN RIJN, Petrus A.
;    TITLE OF INVENTION:  Nucleotide Sequences of Pestivirus
;    TITLE OF INVENTION:  Strains, Polypeptides Encoded by These Sequences and Use
;    TITLE OF INVENTION:  Thereof for Diagnosis and Prevention of Pestivirus
;    TITLE OF INVENTION:  Infections
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  YOUNG & THOMPSON
;      STREET:  745 South 23rd Street
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/750,717
;      FILING DATE:  24-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94201743.5
;      FILING DATE:  17-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/NL95/00214
;      FILING DATE:  16-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PATCH, Andrew J.
;      REGISTRATION NUMBER:  32,925
;      REFERENCE/DOCKET NUMBER:  BO 39123
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-521-2297
;      TELEFAX:  703-685-0573
;      TELEX:  248425 EMBON
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12311 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  374..12067
US-08-750-717-1


  Query Match             72.4%;  Score 15.2;  DB 4;  Length 12311;
  Best Local Similarity   85.0%;  Pred. No. 1.8e+02;
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Db  11877 CTACTTACTAGTCTGTCTGC 11858


RESULT  11
US-08-845-546-1/c
; Sequence 1, Application US/08845546
; Patent No. 6077949
;  GENERAL INFORMATION:
;    APPLICANT:  Munroe, Donald
;    APPLICANT:  Gupta, Ashwani
;    APPLICANT:  Vyas, Tejal
;    APPLICANT:  McCallum, Kirk
;    APPLICANT:  Fan, Ermei
;    TITLE OF INVENTION:  CLONED GLUCAGON-LIKE PEPTIDE
;    TITLE OF INVENTION:  2 RECEPTORS
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
```

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;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/845,546
;      FILING DATE:  24-APR-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Friebel, Thomas E.
;      REGISTRATION NUMBER:  29,258
;      REFERENCE/DOCKET NUMBER:  8607-018
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1574 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  17...1543
;      OTHER INFORMATION:
US-08-845-546-1


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Db     289 CCTTCCTGGGCTCTCTGC 272


RESULT  12
US-08-518-474-7
; Sequence 7, Application US/08518474
; Patent No. 5599920
;  GENERAL INFORMATION:
;    APPLICANT:  Patel, Pragna I.
;    APPLICANT:  Suter, Ueli
;    APPLICANT:  Snipes, G. J.
;    APPLICANT:  Welcher, Andrew
;    APPLICANT:  DeLeon, Marino
;    APPLICANT:  Lupski, James R.
;    APPLICANT:  Shooter, Eric M.
;    TITLE OF INVENTION:  PERIPHERAL MYELIN PROTEIN CODING
;    TITLE OF INVENTION:  SEQUENCE AND METHOD
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/518,474
;      FILING DATE:  21-AUG-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/308,488
;      FILING DATE:  19-SEP-1994
;      APPLICATION NUMBER:  US 07/879,623
;      FILING DATE:  06-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5331-CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5151
;      TELEFAX:  713/651-5246
;      TELEX:  762829
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1736 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-518-474-7


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  Best Local Similarity   88.9%;  Pred. No. 2.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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RESULT  13
US-08-369-043-3
; Sequence 3, Application US/08369043
; Patent No. 5491064
;  GENERAL INFORMATION:
;    APPLICANT:  Lichy, Jack H
;    APPLICANT:  Howley, Peter M
;    TITLE OF INVENTION:  HTS1-Gene, A Human Tumor Suppressor Gene
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend
;      STREET:  1 Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/369,043
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/916,762
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Kenneth A
;      REGISTRATION NUMBER:  31,677
;      REFERENCE/DOCKET NUMBER:  15280-65
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3266 base pairs
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-369-043-3


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  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db   1074 TCCTTCCTGTTCTGCCTG 1091


RESULT  14
US-08-343-443B-24
; Sequence 24, Application US/08343443B
; Patent No. 5968734
;  GENERAL INFORMATION:
;    APPLICANT:  Aurias, Alain
;    APPLICANT:  Delattre, Olivier
;    APPLICANT:  Desmaze, Chantal
;    APPLICANT:  Melot, Thomas
;    APPLICANT:  Peter, Martine
;    APPLICANT:  Plougastel, Beatrice
;    APPLICANT:  Thomas, Gilles
;    APPLICANT:  Zucman, Jessica
;    TITLE OF INVENTION:  NUCLEIC ACID CORRESPONDING TO A GENE OF
;    TITLE OF INVENTION:  CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
;    TITLE OF INVENTION:  TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
;    TITLE OF INVENTION:  TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
;    TITLE OF INVENTION:  TRANSLOCATIONS
;    NUMBER OF SEQUENCES:  129
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Weiser & Associates
;      STREET:  230 South Fifteenth Street
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  AEDIT 1.0 DOS text editor
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/343,443B
;      FILING DATE:  18-NOV-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/FR93/00494
;      FILING DATE:  19-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 92/06123
;      FILING DATE:  20-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  989.6121P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-343-443B-24


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  Best Local Similarity   81.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Db      1 CCTCCTACCAGGTCAGTCTAC 21


RESULT  15
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; Sequence 1, Application US/08681812
; Patent No. 5763593
;  GENERAL INFORMATION:
;    APPLICANT:  Young, Richard A.
;    APPLICANT:  Gadbois, Ellen L.
;    APPLICANT:  Chao, David M.
;    TITLE OF INVENTION:  TBP-Associated Global Negative Regulator
;    TITLE OF INVENTION:  and Methods of Use Thereof
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/681,812
;      FILING DATE:  29-JUL-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI96-07
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  648 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  109..534
US-08-681-812-1


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GenCore version 4.5

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Title: US-09-016-464-18
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Scoring table: IDENTITY_NUC
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	21	100.0	21	14	US-09-016-464-18	Sequence 18, Appl
c 3	21	100.0	51	49	US-60-172-373-19826	Sequence 19826, A
4	21	100.0	81	19	US-09-509-152A-1732	Sequence 1732, Ap
c 5	21	100.0	279	13	US-08-999-861-2798	Sequence 2798, Ap
c 6	21	100.0	279	20	US-09-535-896-10947	Sequence 10947, A
c 7	21	100.0	279	34	US-60-028-852-197	Sequence 197, App
c 8	21	100.0	485	49	US-60-171-481-482	Sequence 482, App
c 9	21	100.0	558	19	US-09-515-128-5435	Sequence 5435, Ap
c 10	21	100.0	601	20	US-09-535-896-15759	Sequence 15759, A
c 11	21	100.0	738	49	US-60-172-373-19824	Sequence 19824, A
c 12	21	100.0	815	49	US-60-172-373-7658	Sequence 7658, Ap
c 13	21	100.0	815	51	US-60-195-106-197	Sequence 197, App
c 14	21	100.0	1278	8	US-08-430-121-17	Sequence 17, Appl
15	21	100.0	7033	19	US-09-509-152A-2411	Sequence 2411, Ap
16	20	95.2	339	16	US-09-234-611-10970	Sequence 10970, A
17	20	95.2	339	16	US-09-289-768-16116	Sequence 16116, A
18	19.4	92.4	505	50	US-60-180-489-1191	Sequence 1191, Ap
c 19	18.4	87.6	191	18	US-09-421-813-102	Sequence 102, App
20	18.4	87.6	362	27	US-09-699-997-5628	Sequence 5628, Ap
21	18.4	87.6	472	55	US-60-236-359-2973	Sequence 2973, Ap
22	18.4	87.6	32768	52	US-60-200-391-42	Sequence 42, Appl
c 23	18	85.7	464	19	US-09-513-991-463	Sequence 463, App
24	17.8	84.8	201	21	US-09-540-229-108754	Sequence 108754,
25	17.8	84.8	262	16	US-09-283-466-3927	Sequence 3927, Ap
26	17.8	84.8	262	17	US-09-304-517A-282082	Sequence 282082,
27	17.8	84.8	298	17	US-09-304-517A-269818	Sequence 269818,
28	17.8	84.8	298	22	US-09-565-240-17996	Sequence 17996, A
29	17.8	84.8	380	17	US-09-304-517A-230787	Sequence 230787,
30	17.8	84.8	380	17	US-09-333-535A-3843	Sequence 3843, Ap
c 31	17.8	84.8	422	25	US-09-652-127-431	Sequence 431, App
32	17.8	84.8	430	40	US-60-089-524-368	Sequence 368, App
33	17.8	84.8	443	19	US-09-528-409-5585	Sequence 5585, Ap
34	17.8	84.8	484	53	US-60-211-750-26467	Sequence 26467, A
c 35	17.8	84.8	498	25	US-09-654-617-407467	Sequence 407467,
c 36	17.8	84.8	498	27	US-09-684-016-407467	Sequence 407467,
c 37	17.8	84.8	500	49	US-60-172-377-3206	Sequence 3206, Ap
38	17.8	84.8	520	25	US-09-654-617-5649	Sequence 5649, Ap
39	17.8	84.8	520	27	US-09-684-016-5649	Sequence 5649, Ap
40	17.8	84.8	619	50	US-60-186-662-440	Sequence 440, App
c 41	17.8	84.8	626	18	US-09-491-404-2088	Sequence 2088, Ap
c 42	17.8	84.8	629	27	US-09-699-998-1202	Sequence 1202, Ap
c 43	17.8	84.8	698	27	US-09-699-998-8453	Sequence 8453, Ap
c 44	17.8	84.8	698	54	US-60-226-326-5164	Sequence 5164, Ap
45	17.8	84.8	713	51	US-60-196-718-2943	Sequence 2943, Ap

ALIGNMENTS

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RESULT   1
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; Sequence 18, Application US/08474497
;  GENERAL INFORMATION:
;    APPLICANT:  Nyce, Jonathan W.
;    TITLE OF INVENTION:  Method of Treatment of Lung Diseases
;    TITLE OF INVENTION:  Using Antisense Oligonucleotides
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  Post Office Drawer 34009
;      CITY:  Charlotte
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,497
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5218-32
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 881-3140
;      TELEFAX:  (919) 881-3175
;      TELEX:  575102
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-474-497-18


  Query Match             100.0%;  Score 21;  DB 8;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db      1 CCTCCTTCCTGGTCTGTCTGC 21


RESULT   2
US-09-016-464-18
; Sequence 18, Application US/09016464
;   GENERAL INFORMATION:
;        APPLICANT: Nyce, Jonathan W.
;        TITLE OF INVENTION: Method of Treatment of Lung Diseases
;                            Using Antisense Oligonucleotides
;        NUMBER OF SEQUENCES: 44
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Kenneth D. Sibley
;             STREET: Post Office Drawer 34009
;             CITY: Charlotte
;             STATE: NC
;             COUNTRY: USA
;             ZIP: 28234
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/016,464
;             FILING DATE: 30-Jan-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/474,497
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sibley, Kenneth D.
;             REGISTRATION NUMBER: 31,665
;             REFERENCE/DOCKET NUMBER: 5218-32
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (919) 881-3140
;             TELEFAX: (919) 881-3175
;             TELEX: 575102
;   INFORMATION FOR SEQ ID NO: 18:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 21 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-016-464-18


  Query Match             100.0%;  Score 21;  DB 14;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db      1 CCTCCTTCCTGGTCTGTCTGC 21


RESULT   3
US-60-172-373-19826/c
; Sequence 19826, Application US/60172373
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT: Lal, Preeti
;  APPLICANT: Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
;  FILE REFERENCE: GX-0006 P
;  CURRENT APPLICATION NUMBER: US/60/172,373
;  CURRENT FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 25,772
;  SOFTWARE: PERL Program
; SEQ ID NO 19826
;   LENGTH: 51
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: SNP00031285
;   FEATURE:
;   NAME/KEY: snp
;   LOCATION: 26
;   OTHER INFORMATION: 444532.1, 443, G->C
US-60-172-373-19826


  Query Match             100.0%;  Score 21;  DB 49;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db     51 CCTCCTTCCTGGTCTGTCTGC 31
```

```
RESULT   4
US-09-509-152A-1732
; Sequence 1732, Application US/09509152A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, JONATHAN W.
;        TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
;                            FORMULATIONS, KITS & APPLICATIONS
;        NUMBER OF SEQUENCES: 2419
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 CLARKE DRIVE
;             CITY: CRANBURY
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/509,152A
;             FILING DATE: 17-Mar-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/059,160
;             FILING DATE: 1997-09-17
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-00991
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1732:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 81 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1732:
US-09-509-152A-1732


  Query Match             100.0%;  Score 21;  DB 19;  Length 81;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db      1 CCTCCTTCCTGGTCTGTCTGC 21


RESULT   5
US-08-999-861-2798/c
; Sequence 2798, Application US/08999861
;  GENERAL INFORMATION:
;    APPLICANT:  Gooding, Douglas H.
;    APPLICANT:  Stuve, Laura L.
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Ito, Laura Y.
;    APPLICANT:  Akerblom, Ingrid E.
;    APPLICANT:  Delegeane, Angelo M.
;    APPLICANT:  Naughton, Rebecca E.
;    APPLICANT:  Klingler, Tod M.
;    TITLE OF INVENTION:  POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
;    TITLE OF INVENTION:  HUMAN UMBILICAL CORD MONONUCLEAR CELLS
;    NUMBER OF SEQUENCES:  3972
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/999,861
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/020,972
;      FILING DATE:  JUNE 28, 1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,852
;      FILING DATE:  OCTOBER 23, 1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CERRONE, MICHAEL C.
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PD-0194 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 855-0555
;      TELEFAX:  (415) 845-4166
;  INFORMATION FOR SEQ ID NO:  2798:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  279 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      CLONE:  1970414H1
US-08-999-861-2798


  Query Match             100.0%;  Score 21;  DB 13;  Length 279;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    228 CCTCCTTCCTGGTCTGTCTGC 208


RESULT   6
US-09-535-896-10947/c
; Sequence 10947, Application US/09535896
; GENERAL INFORMATION:
;  APPLICANT:  Seilhamer, Jeffrey J.
;  APPLICANT:  Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.
;  APPLICANT:  Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.
;  APPLICANT:  Naughton, Rebecca E.
;  TITLE OF INVENTION:  POLYNUCLEOTIDES ENCODING OR REGULATING HYDROLASES
;  FILE REFERENCE:  PD-1003 CIP
;  CURRENT APPLICATION NUMBER: US/09/535,896
;  CURRENT FILING DATE:  2000-03-24
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS:  46268
;  SOFTWARE:  PERL Program
; SEQ ID NO 10947
;   LENGTH: 279
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: hu00056993
;   NAME/KEY: unsure
```

```
;   LOCATION: 42, 109
;   OTHER INFORMATION: a, t, c, g, or other
US-09-535-896-10947


  Query Match             100.0%;  Score 21;  DB 20;  Length 279;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    228 CCTCCTTCCTGGTCTGTCTGC 208


RESULT   7
US-60-028-852-197/c
; Sequence 197, Application US/60028852
;  GENERAL INFORMATION:
;    APPLICANT:  Gooding, Douglas H.
;    APPLICANT:  Stuve, Laura L.
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Ito, Laura Y.
;    APPLICANT:  Akerblom, Ingrid E.
;    APPLICANT:  Delegeane, Angelo M.
;    APPLICANT:  Naughton, Rebecca E.
;    APPLICANT:  Klingler, Tod M.
;    TITLE OF INVENTION:  POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
;    TITLE OF INVENTION:  HUMAN UMBILICAL CORD MONONUCLEAR CELLS
;    NUMBER OF SEQUENCES:  1371
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/028,852
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CERRONE, MICHAEL C.
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PD-0272P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 855-0555
;      TELEFAX:  (415) 845-4166
;  INFORMATION FOR SEQ ID NO:  197:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  279 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      CLONE:  1970414H1
US-60-028-852-197


  Query Match             100.0%;  Score 21;  DB 34;  Length 279;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    228 CCTCCTTCCTGGTCTGTCTGC 208


RESULT   8
US-60-171-481-482/c
; Sequence 482, Application US/60171481
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
;  TITLE OF INVENTION: USES THEREOF
;  FILE REFERENCE: CL000169
;  CURRENT APPLICATION NUMBER: US/60/171,481
;  CURRENT FILING DATE: 1999-12-22
;  NUMBER OF SEQ ID NOS: 1898
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 482
;   LENGTH: 485
;   TYPE: DNA
;   ORGANISM: Human
US-60-171-481-482


  Query Match             100.0%;  Score 21;  DB 49;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    428 CCTCCTTCCTGGTCTGTCTGC 408


RESULT   9
US-09-515-128-5435/c
; Sequence 5435, Application US/09515128
; GENERAL INFORMATION:
;  APPLICANT: Arterburn, Matthew
;  APPLICANT: Asghari, Vida
;  APPLICANT: Damavandi, Simin
;  APPLICANT: Dickson, Mark
;  APPLICANT: Drake, Jim
;  APPLICANT: Drmanac, Radoje
;  APPLICANT: Engleman, Carrie
;  APPLICANT: Faulkner, Brandy
;  APPLICANT: Garcia, Veronica
;  APPLICANT: Giedt, Gretchen
;  APPLICANT: Hunter, Kelly
;  APPLICANT: Jessen, Aaron
;  APPLICANT: Jones, Lee
;  APPLICANT: Kita, David
;  APPLICANT: Labat, Ivan
;  APPLICANT: Laroya, Mimi
;  APPLICANT: Lomelli, Michelle
;  APPLICANT: Nguyen, Phuong
;  APPLICANT: Nogra, Margie
;  APPLICANT: Palencia, Servando
;  APPLICANT: Raisi, Fariba
;  APPLICANT: Smith, Benjamin
;  APPLICANT: Tkach, Joe
;  APPLICANT: Tran, Lien
;  APPLICANT: Verna, Ron
;  APPLICANT: Yang, Fei
;  APPLICANT: Yim, Kenneth
;  TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
;  TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Spleen
;  FILE REFERENCE: 728CIP
;  CURRENT APPLICATION NUMBER: US/09/515,128
;  CURRENT FILING DATE: 2000-02-28
;  EARLIER APPLICATION NUMBER: 09/034,341
;  EARLIER FILING DATE: 1998-02-13
;  NUMBER OF SEQ ID NOS: 24489
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5435
;   LENGTH: 558
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

```
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(558)
;   OTHER INFORMATION: n = A,T,C or G
US-09-515-128-5435


  Query Match             100.0%;  Score 21;  DB 19;  Length 558;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    472 CCTCCTTCCTGGTCTGTCTGC 452


RESULT  10
US-09-535-896-15759/c
; Sequence 15759, Application US/09535896
; GENERAL INFORMATION:
;  APPLICANT:  Seilhamer, Jeffrey J.
;  APPLICANT:  Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.
;  APPLICANT:  Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.
;  APPLICANT:  Naughton, Rebecca E.
;  TITLE OF INVENTION:  POLYNUCLEOTIDES ENCODING OR REGULATING HYDROLASES
;  FILE REFERENCE:  PD-1003 CIP
;  CURRENT APPLICATION NUMBER: US/09/535,896
;  CURRENT FILING DATE:  2000-03-24
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS:  46268
;  SOFTWARE:  PERL Program
; SEQ ID NO 15759
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: hu01099445
US-09-535-896-15759


  Query Match             100.0%;  Score 21;  DB 20;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    442 CCTCCTTCCTGGTCTGTCTGC 422


RESULT  11
US-60-172-373-19824/c
; Sequence 19824, Application US/60172373
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT: Lal, Preeti
;  APPLICANT: Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymorp
;  FILE REFERENCE: GX-0006 P
;  CURRENT APPLICATION NUMBER: US/60/172,373
;  CURRENT FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 25,772
;  SOFTWARE: PERL Program
; SEQ ID NO 19824
;   LENGTH: 738
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 444532.1
US-60-172-373-19824


  Query Match             100.0%;  Score 21;  DB 49;  Length 738;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    468 CCTCCTTCCTGGTCTGTCTGC 448


RESULT  12
US-60-172-373-7658/c
; Sequence 7658, Application US/60172373
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT: Lal, Preeti
;  APPLICANT: Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
;  FILE REFERENCE: GX-0006 P
;  CURRENT APPLICATION NUMBER: US/60/172,373
;  CURRENT FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 25,772
;  SOFTWARE: PERL Program
; SEQ ID NO 7658
;   LENGTH: 815
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 444532.3
US-60-172-373-7658


  Query Match             100.0%;  Score 21;  DB 49;  Length 815;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    565 CCTCCTTCCTGGTCTGTCTGC 545


RESULT  13
US-60-195-106-197/c
; Sequence 197, Application US/60195106
; GENERAL INFORMATION:
;  APPLICANT:  Shiffman, Dov
;  APPLICANT:  Somogyi, Roland
;  APPLICANT:  Lawn, Richard M.
;  APPLICANT:  Seilhamer, Jeffrey J.
;  APPLICANT:  Porter, Gordon J.
;  APPLICANT:  Mikita, Thomas
;  APPLICANT:  Tai, Julie T.N.
;  TITLE OF INVENTION:  GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
;  FILE REFERENCE:  PA-0025 P
;  CURRENT APPLICATION NUMBER: US/60/195,106
;  CURRENT FILING DATE:  2000-04-05
;  NUMBER OF SEQ ID NOS:  276
;  SOFTWARE:  PERL Program
; SEQ ID NO 197
;   LENGTH: 815
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 997377.1
US-60-195-106-197


  Query Match             100.0%;  Score 21;  DB 51;  Length 815;
```

```
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTGC 21
           |||||||||||||||||||||
Db     565 CCTCCTTCCTGGTCTGTCTGC 545


RESULT  14
US-08-430-121-17/c
; Sequence 17, Application US/08430121
;  GENERAL INFORMATION:
;    APPLICANT:  Simonsen, Christian C.
;    APPLICANT:  McGrogan, Michael
;    TITLE OF INVENTION:  Recombinant Products of an Eosinophilic
;    TITLE OF INVENTION:  Gene Family
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,121
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,859
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/630,976
;      FILING DATE:  19-DEC-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Shetka, Debra A.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  24842-20058.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-813-5600
;      TELEFAX:  415-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1278 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-430-121-17


  Query Match             100.0%;  Score 21;  DB 8;  Length 1278;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTGC 21
           |||||||||||||||||||||
Db     951 CCTCCTTCCTGGTCTGTCTGC 931


RESULT  15
US-09-509-152A-2411
; Sequence 2411, Application US/09509152A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, JONATHAN W.
;        TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
;                            FORMULATIONS, KITS & APPLICATIONS
;        NUMBER OF SEQUENCES: 2419
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 CLARKE DRIVE
;             CITY: CRANBURY
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/509,152A
;             FILING DATE: 17-Mar-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/059,160
;             FILING DATE: 1997-09-17
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-00991
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2411:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 7033 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2411:
US-09-509-152A-2411


  Query Match             100.0%;  Score 21;  DB 19;  Length 7033;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTGC 21
           |||||||||||||||||||||
Db       1 CCTCCTTCCTGGTCTGTCTGC 21


Search completed: April 20, 2001, 03:21:25
Job time: 14172 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:15:40 ; Search time 101.94 Seconds
(without alignments)
28.506 Million cell updates/sec

Title: US-09-016-464-18
Perfect score: 21
Sequence: 1 CCTCCTTCCTGGTCTGTCTGC 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 46985 seqs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	81	5	US-09-543-679A-1732	Sequence 1732, Ap
c	2	21	100.0	715	5	US-09-543-679A-2861	Sequence 2861, Ap
c	3	21	100.0	718	5	US-09-543-679A-2860	Sequence 2860, Ap
c	4	21	100.0	1452	5	US-09-543-679A-2862	Sequence 2862, Ap
c	5	21	100.0	2885	5	US-09-543-679A-2863	Sequence 2863, Ap
	6	21	100.0	7033	5	US-09-543-679A-2411	Sequence 2411, Ap
	7	21	100.0	209274	5	US-09-543-679A-3004	Sequence 3004, Ap
	8	17.4	82.9	11579	6	US-60-248-505-470	Sequence 470, App
	9	16.8	80.0	562	1	PCT-US01-01350-37	Sequence 37, Appl
c	10	16.4	78.1	98744	6	US-60-248-505-30	Sequence 30, Appl
	11	16.2	77.1	289	4	US-08-276-163D-12910	Sequence 12910, A
c	12	16.2	77.1	509	4	US-08-276-163D-1918	Sequence 1918, Ap
	13	16.2	77.1	13491	6	US-60-248-505-337	Sequence 337, App
	14	16.2	77.1	21287	6	US-60-248-505-415	Sequence 415, App
c	15	16.2	77.1	124647	6	US-60-248-505-285	Sequence 285, App
	16	16.2	77.1	203032	6	US-60-248-505-308	Sequence 308, App
c	17	15.8	75.2	408	4	US-08-276-163D-1780	Sequence 1780, Ap
c	18	15.8	75.2	504	4	US-08-276-163D-14029	Sequence 14029, A
c	19	15.8	75.2	771	5	US-09-739-449-8040	Sequence 8040, Ap
c	20	15.8	75.2	850	5	US-09-739-449-2264	Sequence 2264, Ap
	21	15.8	75.2	56642	6	US-60-248-505-263	Sequence 263, App
	22	15.8	75.2	56643	6	US-60-248-505-572	Sequence 572, App
	23	15.4	73.3	510	4	US-08-276-163D-8563	Sequence 8563, Ap
	24	15.2	72.4	436	1	PCT-US01-01351-595	Sequence 595, App
	25	15.2	72.4	722	6	US-60-248-505-1445	Sequence 1445, Ap
c	26	15.2	72.4	1375	6	US-60-248-505-1983	Sequence 1983, Ap
	27	15.2	72.4	2004	5	US-09-739-449-6218	Sequence 6218, Ap
c	28	15.2	72.4	2674	5	US-09-817-199-1	Sequence 1, Appli
c	29	15.2	72.4	9685	6	US-60-248-505-113	Sequence 113, App
c	30	15.2	72.4	13182	5	US-09-817-199-3	Sequence 3, Appli
	31	15.2	72.4	20341	6	US-60-248-505-651	Sequence 651, App
	32	15.2	72.4	32696	6	US-60-248-505-281	Sequence 281, App
c	33	15.2	72.4	33702	6	US-60-248-505-465	Sequence 465, App
	34	15.2	72.4	54477	6	US-60-248-505-143	Sequence 143, App
c	35	15.2	72.4	64927	6	US-60-248-505-262	Sequence 262, App
	36	15.2	72.4	88789	5	US-09-739-449-199	Sequence 199, App
	37	15.2	72.4	283061	6	US-60-248-505-134	Sequence 134, App
c	38	15.2	72.4	449171	6	US-60-248-505-42	Sequence 42, Appl
c	39	15	71.4	213456	5	US-09-820-007-3	Sequence 3, Appli
	40	15	71.4	239630	6	US-60-248-505-158	Sequence 158, App
	41	14.8	70.5	396	5	US-09-442-385-339	Sequence 339, App
c	42	14.8	70.5	499	4	US-08-276-163D-13266	Sequence 13266, A
	43	14.8	70.5	5123	6	US-60-248-505-117	Sequence 117, App
c	44	14.8	70.5	13295	6	US-60-248-505-348	Sequence 348, App
c	45	14.8	70.5	13769	6	US-60-248-505-385	Sequence 385, App

ALIGNMENTS

```
RESULT   1
US-09-543-679A-1732
; Sequence 1732, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1732:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 81 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1732:
US-09-543-679A-1732


  Query Match            100.0%;  Score 21;  DB 5;  Length 81;
  Best Local Similarity  100.0%;  Pred. No. 0.34;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1 CCTCCTTCCTGGTCTGTCTGC 21
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Db       1 CCTCCTTCCTGGTCTGTCTGC 21


RESULT   2
US-09-543-679A-2861/c
; Sequence 2861, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2861:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 715 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2861:
US-09-543-679A-2861


  Query Match             100.0%;  Score 21;  DB 5;  Length 715;
  Best Local Similarity   100.0%;  Pred. No. 0.42;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTGC 21
           |||||||||||||||||||||
Db     450 CCTCCTTCCTGGTCTGTCTGC 430


RESULT   3
US-09-543-679A-2860/c
; Sequence 2860, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2860:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 718 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2860:
US-09-543-679A-2860


  Query Match             100.0%;  Score 21;  DB 5;  Length 718;
  Best Local Similarity   100.0%;  Pred. No. 0.42;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCTTCCTGGTCTGTCTGC 21
           |||||||||||||||||||||
Db     448 CCTCCTTCCTGGTCTGTCTGC 428


RESULT   4
US-09-543-679A-2862/c
; Sequence 2862, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
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;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2862:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1452 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2862:
US-09-543-679A-2862


  Query Match            100.0%;  Score 21;  DB 5;  Length 1452;
  Best Local Similarity  100.0%;  Pred. No. 0.45;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db    951 CCTCCTTCCTGGTCTGTCTGC 931


RESULT   5
US-09-543-679A-2863/c
; Sequence 2863, Application US/09543679A
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2863:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2885 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2863:
US-09-543-679A-2863


  Query Match            100.0%;  Score 21;  DB 5;  Length 2885;
  Best Local Similarity  100.0%;  Pred. No. 0.48;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db   2384 CCTCCTTCCTGGTCTGTCTGC 2364


RESULT   6
US-09-543-679A-2411
; Sequence 2411, Application US/09543679A
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2411:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 7033 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2411:
US-09-543-679A-2411


  Query Match            100.0%;  Score 21;  DB 5;  Length 7033;
  Best Local Similarity  100.0%;  Pred. No. 0.53;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db      1 CCTCCTTCCTGGTCTGTCTGC 21


RESULT   7
US-09-543-679A-3004
; Sequence 3004, Application US/09543679A
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
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```
;                          COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                          OF AIRWAY DISORDERS ASSOCIATED WITH
;                          BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3004:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 209274 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3004:
US-09-543-679A-3004


  Query Match           100.0%;  Score 21;  DB 5;  Length 209274;
  Best Local Similarity  100.0%;  Pred. No. 0.74;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||||||||||||||||||
Db      1 CCTCCTTCCTGGTCTGTCTGC 21


RESULT   8
US-60-248-505-470
; Sequence 470, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: cl000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 470
;   LENGTH: 11579
;   TYPE: DNA
;   ORGANISM: human
US-60-248-505-470


  Query Match           82.9%;  Score 17.4;  DB 6;  Length 11579;
  Best Local Similarity  94.7%;  Pred. No. 21;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 TCCTTCCTGGTCTGTCTGC 21
          || |||||||||||||||||
Db   5449 tcattcctggtctgtctgc 5467


RESULT   9
PCT-US01-01350-37
; Sequence 37, Application PC/TUS0101350
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc., et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PA110PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/01350
;  CURRENT FILING DATE:  2001-03-17
;  NUMBER OF SEQ ID NOS: 334
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
;   LENGTH: 562
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US01-01350-37


  Query Match           80.0%;  Score 16.8;  DB 1;  Length 562;
  Best Local Similarity  90.0%;  Pred. No. 29;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 CTCCTTCCTGGTCTGTCTGC 21
          | || |||||||||||||||
Db    474 ccccatcctggtctgtctgc 493


RESULT  10
US-60-248-505-30/c
; Sequence 30, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: cl000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
;   LENGTH: 98744
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(98744)
;   OTHER INFORMATION: n = A,T,C or G
US-60-248-505-30


  Query Match           78.1%;  Score 16.4;  DB 6;  Length 98744;
  Best Local Similarity  94.4%;  Pred. No. 70;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 TCCTTCCTGGTCTGTCTG 20
          ||| ||||||||||||||
Db   9032 TCCATCCTGGTCTGTCTG 9015


RESULT  11
US-08-276-163D-12910
; Sequence 12910, Application US/08276163D
; GENERAL INFORMATION:
;  APPLICANT: Adams, et. al.
;  TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
;  FILE REFERENCE: PO14
```

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;  CURRENT APPLICATION NUMBER: US/08/276,163D
;  CURRENT FILING DATE:  1994-07-15
;  NUMBER OF SEQ ID NOS: 15314
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12910
;   LENGTH: 289
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (51)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (156)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (270)
;   OTHER INFORMATION: n equals a,t,g, or c
US-08-276-163D-12910


  Query Match            77.1%;  Score 16.2;  DB 4;  Length 289;
  Best Local Similarity   85.7%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          ||||| ||| |||||||| ||
Db     69 cctccatccaggtctgtcagc 89


RESULT  12
US-08-276-163D-1918/c
; Sequence 1918, Application US/08276163D
; GENERAL INFORMATION:
;  APPLICANT: Adams, et. al.
;  TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
;  FILE REFERENCE: PO14
;  CURRENT APPLICATION NUMBER: US/08/276,163D
;  CURRENT FILING DATE:  1994-07-15
;  NUMBER OF SEQ ID NOS: 15314
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1918
;   LENGTH: 509
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (8)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (33)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (112)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (138)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (144)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (347)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (376)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (402)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (404)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (410)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (425)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (428)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
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;   NAME/KEY: misc feature
;   LOCATION: (437)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (441)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (445)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (456)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (465)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (485)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (490)
;   OTHER INFORMATION: n equals a,t,g, or c
US-08-276-163D-1918


  Query Match            77.1%;  Score 16.2;  DB 4;  Length 509;
  Best Local Similarity   85.7%;  Pred. No. 52;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          | |||||||| |||||| |||
Db    174 CTTCCTTCCTTGTCTGTTTGC 154


RESULT  13
US-60-248-505-337
; Sequence 337, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: cl000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 337
;   LENGTH: 13491
;   TYPE: DNA
;   ORGANISM: human
US-60-248-505-337


  Query Match            77.1%;  Score 16.2;  DB 6;  Length 13491;
  Best Local Similarity   85.7%;  Pred. No. 72;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          ||||| ||||| ||| |||||
Db   7801 cctccctcctgttctctctgc 7821
```

```
RESULT  14
US-60-248-505-415
; Sequence 415, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: cl000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 415
;   LENGTH: 21287
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(21287)
;   OTHER INFORMATION: n = A,T,C or G
US-60-248-505-415


  Query Match             77.1%;  Score 16.2;  DB 6;  Length 21287;
  Best Local Similarity   85.7%;  Pred. No. 75;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          ||||| ||||| ||| |||||
Db  16179 cctccctcctgttctctctgc 16199


RESULT  15
US-60-248-505-285/c
; Sequence 285, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: cl000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 285
;   LENGTH: 124647
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(124647)
;   OTHER INFORMATION: n = A,T,C or G
US-60-248-505-285


  Query Match             77.1%;  Score 16.2;  DB 6;  Length 124647;
  Best Local Similarity   85.7%;  Pred. No. 86;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCTCCTTCCTGGTCTGTCTGC 21
          |||||| ||||| || |||||
Db  69282 CCTCCTCCCTGGCCTCTCTGC 69262


Search completed: April 20, 2001, 00:15:48
Job time: 9485 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:00:28 ; Search time 2028.86 Seconds
(without alignments)
60.703 Million cell updates/sec

Title: US-09-016-464-19
Perfect score: 20
Sequence: 1 GCCCTGCTGCTCTTTCTGCT 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
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17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
21: em_htgo_rod:*
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23: em_htg_hum2:*
24: em_htg_hum3:*
25: em_htg_hum4:*
26: em_htg_hum5:*
27: em_htg_hum6:*
28: em_htg_hum7:*
29: em_htg_hum8:*
30: em_htg_inv1:*
31: em_htg_inv2:*
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33: em_htg_rod:*
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91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_ro1:*
95: gb_ro2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	1199	88	AF294027	AF294027 Pan trogl
c	2	20	100.0	1199	88	AF294028	AF294028 Pan trogl
c	3	20	100.0	1203	88	AF294019	AF294019 Homo sapi
c	4	20	100.0	1203	88	AF294020	AF294020 Homo sapi
c	5	20	100.0	1203	88	AF294021	AF294021 Homo sapi
c	6	20	100.0	1203	88	AF294022	AF294022 Homo sapi
c	7	20	100.0	1203	88	AF294023	AF294023 Homo sapi
c	8	20	100.0	1203	88	AF294024	AF294024 Homo sapi
c	9	20	100.0	1203	88	AF294025	AF294025 Homo sapi
c	10	20	100.0	1203	88	AF294026	AF294026 Homo sapi
c	11	20	100.0	1214	88	AF294007	AF294007 Homo sapi

c	12	20	100.0	1214	88	AF294008	AF294008 Homo sapi
c	13	20	100.0	1214	88	AF294009	AF294009 Homo sapi
c	14	20	100.0	1214	88	AF294010	AF294010 Homo sapi
c	15	20	100.0	1214	88	AF294011	AF294011 Homo sapi
c	16	20	100.0	1214	88	AF294012	AF294012 Homo sapi
c	17	20	100.0	1214	88	AF294013	AF294013 Homo sapi
c	18	20	100.0	1214	88	AF294014	AF294014 Homo sapi
c	19	20	100.0	1214	88	AF294015	AF294015 Homo sapi
c	20	20	100.0	1214	88	AF294016	AF294016 Pan trogl
c	21	20	100.0	1214	88	AF294017	AF294017 Pan trogl
c	22	20	100.0	1214	88	AF294018	AF294018 Pan trogl
c	23	20	100.0	1347	91	HHSECRPG	X55989 Human ECRP
c	24	20	100.0	1452	92	HSECP1	X16545 Human DNA f
c	25	20	100.0	1489	92	HSEOSDN	X16546 Human DNA f
c	26	20	100.0	1501	92	HSEDNG	X55987 Human EDN g
c	27	20	100.0	1669	92	HSECPG	X55990 Human ECP g
c	28	20	100.0	4050	91	D86343	D86343 Homo sapien
	29	20	100.0	157981	83	CNS05TD4	AL355922 Homo sapi
c	30	20	100.0	162472	83	CNS01DUW	AL133371 Homo sapi
c	31	19	95.0	142260	79	AL353892	AL353892 Homo sapi
	32	19	95.0	165930	67	AC021401	AC021401 Homo sapi
c	33	19	95.0	210837	64	AC016432	AC016432 Homo sapi
	34	18.4	92.0	57056	82	AP000637	AP000637 Homo sapi
	35	18.4	92.0	184555	76	AC078961	AC078961 Homo sapi
c	36	18.4	92.0	190191	66	AC019077	AC019077 Homo sapi
	37	18.4	92.0	193170	74	AC068652	AC068652 Mus muscu
c	38	18	90.0	118338	87	AC010463	AC010463 Homo sapi
c	39	18	90.0	163401	75	AC073251	AC073251 Homo sapi
c	40	18	90.0	179141	66	AC019091	AC019091 Homo sapi
c	41	18	90.0	274095	63	AC012295	AC012295 Mus muscu
c	42	17.4	87.0	5652	66	AC020212	AC020212 Drosophil
c	43	17.4	87.0	45000	85	AB039887	AB039887 Homo sapi
c	44	17.4	87.0	47919	64	AC015044	AC015044 Drosophil
	45	17.4	87.0	84871	92	HSDJ54G6	AL121588 Human DNA

ALIGNMENTS

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RESULT   1
AF294027/c
LOCUS       AF294027     1199 bp    DNA             PRI       19-DEC-2000
DEFINITION  Pan troglodytes haplotype 1 eosinophil cationic protein (ECP) gene,
            complete cds.
ACCESSION   AF294027
VERSION     AF294027.1  GI:9954419
KEYWORDS    .
SOURCE      chimpanzee.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1199)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1199)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1199
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /haplotype="1"
     mRNA            join(<209. .276,503. .1169)
                     /gene="ECP"
                     /product="eosinophil cationic protein"
     gene            <209. .1169
                     /gene="ECP"
     CDS             508. .990
                     /gene="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG09050.1"
                     /db_xref="GI:9954420"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRVINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHQSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDATI
                     "
BASE COUNT      308 a    305 c    292 g    294 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 88;  Length 1199;
  Best Local Similarity  100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT   2
AF294028/c
LOCUS       AF294028     1199 bp    DNA             PRI       19-DEC-2000
DEFINITION  Pan troglodytes haplotype 2 eosinophil cationic protein (ECP) gene,
            complete cds.
ACCESSION   AF294028
VERSION     AF294028.1  GI:9954421
KEYWORDS    .
SOURCE      chimpanzee.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1199)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1199)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1199
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /haplotype="2"
     mRNA            join(<209. .276,503. .1169)
                     /gene="ECP"
                     /product="eosinophil cationic protein"
     gene            <209. .1169
                     /gene="ECP"
     CDS             508. .990
                     /gene="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG09051.1"
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                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRVINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHQSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDATI
                     "
BASE COUNT      308 a    306 c    292 g    293 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 88;  Length 1199;
  Best Local Similarity  100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 GCCCTGCTGCTCTTTCTGCT 20
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Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT   3
AF294019/c
LOCUS       AF294019     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 1 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294019
VERSION     AF294019.1  GI:11139039
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="1"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31589.1"
                     /db_xref="GI:11139040"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCTYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      317 a    306 c    285 g    295 t
ORIGIN


  Query Match            100.0%;  Score 20;  DB 88;  Length 1203;
  Best Local Similarity  100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT   4
AF294020/c
LOCUS       AF294020     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 2 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294020
VERSION     AF294020.1  GI:11139041
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="2"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31590.1"
                     /db_xref="GI:11139042"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      318 a    303 c    287 g    295 t
ORIGIN


  Query Match            100.0%;  Score 20;  DB 88;  Length 1203;
  Best Local Similarity  100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT   5
AF294021/c
LOCUS       AF294021     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 3 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294021
VERSION     AF294021.1  GI:11139043
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
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  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
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                     /db_xref="taxon:9606"
                     /haplotype="3"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31591.1"
                     /db_xref="GI:11139044"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCTYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      317 a    305 c    286 g    295 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT   6
AF294022/c
LOCUS       AF294022     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 4 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294022
VERSION     AF294022.1  GI:11139045
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
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                     /db_xref="taxon:9606"
                     /haplotype="4"
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                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
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                     /protein_id="AAG31592.1"
                     /db_xref="GI:11139046"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      317 a    304 c    287 g    295 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT   7
AF294023/c
LOCUS       AF294023     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 5 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294023
VERSION     AF294023.1  GI:11139047
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="5"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
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                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
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                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      316 a    304 c    287 g    296 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT   8
AF294024/c
LOCUS       AF294024     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 6 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294024
VERSION     AF294024.1  GI:11139049
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
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                     /db_xref="taxon:9606"
                     /haplotype="6"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31594.1"
                     /db_xref="GI:11139050"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      317 a    303 c    287 g    296 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT   9
AF294025/c
LOCUS       AF294025     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 7 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294025
VERSION     AF294025.1  GI:11139051
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="7"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31595.1"
                     /db_xref="GI:11139052"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
                     LNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSR
                     FRVPLLHCDLINPGAQNISNCTYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      317 a    304 c    286 g    296 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT  10
AF294026/c
LOCUS       AF294026     1203 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 8 eosinophil cationic protein gene, complete
            cds.
ACCESSION   AF294026
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VERSION     AF294026.1  GI:11139053
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1203)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="8"
     mRNA            join(209. .276,507. .1173)
                     /product="eosinophil cationic protein"
     exon            209. .276
                     /number=1
     5'UTR           join(209. .276,507. .511)
     intron          277. .506
                     /number=1
     exon            507. .1173
                     /number=2
     CDS             512. .994
                     /note="ECP"
                     /codon_start=1
                     /product="eosinophil cationic protein"
                     /protein_id="AAG31596.1"
                     /db_xref="GI:11139054"
                     /translation="MVPKLFTSQICLLLLLGLMGVEGSLHARPPQFTRAQWFAIQHIS
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                     FRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI
                     "
     3'UTR           995. .1173
BASE COUNT      316 a    305 c    287 g    295 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 88;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT  11
AF294007/c
LOCUS       AF294007     1214 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 1 eosinophil-derived neurotoxin gene,
            complete cds.
ACCESSION   AF294007
VERSION     AF294007.1  GI:11139015
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1214)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1214)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1214
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="1"
     mRNA            join(245. .314,541. .1209)
                     /product="eosinophil-derived neurotoxin"
     5'UTR           join(245. .314,541. .545)
     exon            245. .314
                     /number=1
     intron          315. .540
                     /number=1
     exon            541. .1209
                     /number=2
     CDS             546. .1031
                     /note="EDN; eosinophil-associated ribonuclease"
                     /codon_start=1
                     /product="eosinophil-derived neurotoxin"
                     /protein_id="AAG31577.1"
                     /db_xref="GI:11139016"
                     /translation="MVPKLFTSQICLLLLLGLLAVEGSLHVKPPQFTWAQWFETQHIN
                     MTSQQCTNAMQVINNYQRRCKNQNTFLLTTFANVVNVCGNPNMTCPSNKTRKNCHHSG
                     SQVPLIHCNLTTPSPQNISNCRYAQTPANMFYIVACDNRDQRRDPPQYPVVPVHLDRI
                     I"
     3'UTR           1032. .1209
BASE COUNT      341 a    317 c    264 g    292 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 88;  Length 1214;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT  12
AF294008/c
LOCUS       AF294008     1214 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 2 eosinophil-derived neurotoxin gene,
            complete cds.
ACCESSION   AF294008
VERSION     AF294008.1  GI:11139017
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1214)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1214)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1214
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                     /db_xref="taxon:9606"
                     /haplotype="2"
     mRNA            join(245. .314,541. .1209)
                     /product="eosinophil-derived neurotoxin"
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     5'UTR           join(245. .314,541. .545)
     exon            245. .314
                     /number=1
     intron          315. .540
                     /number=1
     exon            541. .1209
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                     /note="EDN; eosinophil-associated ribonuclease"
                     /codon_start=1
                     /product="eosinophil-derived neurotoxin"
                     /protein_id="AAG31578.1"
                     /db_xref="GI:11139018"
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                     SQVPLIHCNLTTPSPQNISNCRYAQTPANMFYIVACDNRDQRRDPPQYPVVPVHLDRI
                     I"
     3'UTR           1032. .1209
BASE COUNT      341 a    318 c    263 g    292 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 88;  Length 1214;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT  13
AF294009/c
LOCUS       AF294009     1214 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 3 eosinophil-derived neurotoxin gene,
            complete cds.
ACCESSION   AF294009
VERSION     AF294009.1  GI:11139019
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1214)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1214)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1214
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                     /db_xref="taxon:9606"
                     /haplotype="3"
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     5'UTR           join(245. .314,541. .545)
     exon            245. .314
                     /number=1
     intron          315. .540
                     /number=1
     exon            541. .1209
                     /number=2
     CDS             546. .1031
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                     /codon_start=1
                     /product="eosinophil-derived neurotoxin"
                     /protein_id="AAG31579.1"
                     /db_xref="GI:11139020"
                     /translation="MVPKLFTSQICLLLLLGLLAVEGSLHVKPPQFTWAQWFETQHIN
                     MTSQQCTNAMQVINNYQRRCKNQNTFLLTTFANVVNVCGNPNMTCPSNKTRKNCHHSG
                     SQVPLIHCNLTTPSPQNISNCRYAQTPANMFYIVACDNRDQRRDPPQYPVVPVHLDRI
                     I"
     3'UTR           1032. .1209
BASE COUNT      341 a    318 c    264 g    291 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 88;  Length 1214;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT  14
AF294010/c
LOCUS       AF294010     1214 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 4 eosinophil-derived neurotoxin gene,
            complete cds.
ACCESSION   AF294010
VERSION     AF294010.1  GI:11139021
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1214)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1214)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1214
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="4"
     mRNA            join(245. .314,541. .1209)
                     /product="eosinophil-derived neurotoxin"
     5'UTR           join(245. .314,541. .545)
     exon            245. .314
                     /number=1
     intron          315. .540
                     /number=1
     exon            541. .1209
                     /number=2
     CDS             546. .1031
                     /note="EDN; eosinophil-associated ribonuclease"
                     /codon_start=1
                     /product="eosinophil-derived neurotoxin"
                     /protein_id="AAG31580.1"
                     /db_xref="GI:11139022"
                     /translation="MVPKLFTSQICLLLLLGLLAVEGSLHVKPPQFTWAQWFETQHIN
                     MTSQQCTNAMQVINNYQRRCKNQNTFLLTTFANVVNVCGNPNMTCPSNKTRKNCHHSG
                     SQVPLIHCNLTTPSPQNISNCRYAQTPANMFYIVACDNRDQRRDPPQYPVVPVHLDRI
                     I"
     3'UTR           1032. .1209
BASE COUNT      340 a    316 c    265 g    293 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 88;  Length 1214;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
```

```
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


RESULT  15
AF294011/c
LOCUS       AF294011     1214 bp    DNA             PRI       19-DEC-2000
DEFINITION  Homo sapiens haplotype 5 eosinophil-derived neurotoxin gene,
            complete cds.
ACCESSION   AF294011
VERSION     AF294011.1  GI:11139023
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1214)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Sequence Variation at Two Eosinophil-Associated Ribonuclease Loci
            in Humans
  JOURNAL   Genetics 156 (4), 1949-1958 (2000)
   PUBMED   11102386
REFERENCE   2  (bases 1 to 1214)
  AUTHORS   Zhang,J. and Rosenberg,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2000) LHD/NIAID/NIH, Building 10, Room 11N104,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1214
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /haplotype="5"
     mRNA            join(245. .314,541. .1209)
                     /product="eosinophil-derived neurotoxin"
     5'UTR           join(245. .314,541. .545)
     exon            245. .314
                     /number=1
     intron          315. .540
                     /number=1
     exon            541. .1209
                     /number=2
     CDS             546. .1031
                     /note="EDN; eosinophil-associated ribonuclease"
                     /codon_start=1
                     /product="eosinophil-derived neurotoxin"
                     /protein_id="AAG31581.1"
                     /db_xref="GI:11139024"
                     /translation="MVPKLFTSQICLLLLLGLLAVEGSLHVKPPQFTWAQWFETQHIN
                     MTSQQCTNAMQVINNYQRRCKNQNTFLLTTFANVVNVCGNPNMTCPSNKTRKNCHHSG
                     SQVPLIHCNLTTPSPQNISNCRYAQTPANMFYIVACDNRDQRRDPPQYPVVPVHLDRI
                     I"
     3'UTR           1032. .1209
BASE COUNT      341 a    318 c    264 g    291 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 88;  Length 1214;
  Best Local Similarity  100.0%;  Pred. No. 9.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     66 GCCCTGCTGCTCTTTCTGCT 47


Search completed: April 20, 2001, 00:00:29
Job time: 9506 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:12:59 ; Search time 547.68 Seconds
(without alignments)
21.318 Million cell updates/sec

Title: US-09-016-464-19
Perfect score: 20
Sequence: 1 GCCCTGCTGCTCTTTCTGCT 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	18	T76120	Human eosinophil d
	2	20	100.0	20	20	X53926	Eosinophil derived
	3	20	100.0	20	21	F19488	Human eosinophil d
	4	20	100.0	20	21	A33366	Low adenosine anti
	5	20	100.0	156	20	X54599	Eosinophil derived
	6	20	100.0	156	21	F20168	Human eosinophil d
	7	20	100.0	156	21	A34046	Human adenosine re
c	8	20	100.0	1452	21	F21295	Human low adenosin
c	9	20	100.0	1452	21	A35173	Human adenosine re
c	10	20	100.0	1489	21	F21298	Human low adenosin
c	11	20	100.0	1489	21	A35176	Human adenosine re
c	12	20	100.0	2885	21	F21296	Human low adenosin
c	13	20	100.0	2885	21	A35174	Human adenosine re
c	14	20	100.0	2918	21	F21300	Human low adenosin
c	15	20	100.0	2918	21	A35178	Human adenosine re
	16	20	100.0	7033	21	F20844	Human low adenosin
	17	20	100.0	7033	21	A34722	Human adenosine re
	18	20	100.0	7036	20	X55274	Human factor-relat
	19	20	100.0	114955	20	X53491	Human adenosine A1
	20	20	100.0	209273	21	F21437	Human factor-relat
	21	16.8	84.0	1788	21	Z50894	Human receptor-ass
	22	16.8	84.0	2156	12	Q11562	Partial endothelia
	23	16.8	84.0	24978	20	X60209	SEQ ID 3 of US5914
	24	16.8	84.0	24979	21	A52321	Genomic DNA sequen
	25	16.4	82.0	112	16	T25011	Human gene signatu
	26	16.4	82.0	483	21	Z53900	Neisseria gonorrhe
	27	16.4	82.0	483	21	Z53901	Neisseria meningit
	28	16.4	82.0	483	21	Z53902	Neisseria meningit
c	29	16.4	82.0	492	20	X25393	Streptococcus pneu
c	30	16.4	82.0	504	21	A08556	S. pneumoniae 20 k
	31	16.4	82.0	527	21	C50576	Arabidopsis thalia
	32	16.4	82.0	529	21	C34033	Arabidopsis thalia
	33	16.4	82.0	568	21	C36175	Arabidopsis thalia
c	34	16.4	82.0	656	21	F12854	Aspergillus oryzae
	35	16.4	82.0	938	21	C54851	Arabidopsis thalia
	36	16.4	82.0	941	21	C52389	Arabidopsis thalia
	37	16.4	82.0	1273	21	Z61417	DNA encoding the l
c	38	16.4	82.0	2163	20	X25394	Streptococcus pneu
c	39	16.4	82.0	2290	19	V27356	Streptococcus pneu
c	40	16.4	82.0	2359	19	V52376	Streptococcus pneu
c	41	16.4	82.0	2478	21	A08557	S. pneumoniae 92 k
c	42	16.4	82.0	2481	21	A05417	Streptococcus pneu
c	43	16.4	82.0	2523	21	A65731	Streptococcus pneu
c	44	16.4	82.0	2531	21	A47602	Recombinant varian
c	45	16.4	82.0	2531	21	A47605	Recombinant varian

ALIGNMENTS

RESULT 1
T76120
ID T76120 standard; DNA; 20 BP.
XX
AC T76120;
XX
DT 12-SEP-1997 (first entry)
XX
DE Human eosinophil derived neurotoxin antisense oligonucleotide.
XX
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; ss.
XX
OS Synthetic.
XX
PN WO9640162-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09306.
XX
PR 07-JUN-1995; 95US-0474497.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Metzger WJ, Nyce JW;
XX
DR WPI; 1997-051871/05.
XX
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject
XX
PS Claim 5; Page 27; 71pp; English.

```
XX
CC   A method for treating airway disease in a subject has been produced,
CC   which involves the topical administration of an essentially adenosine
CC   free antisense oligonucleotide (ON) to the airway epithelium of the
CC   subject. The present sequence is an antisense oligonucleotide
CC   HSEOSDNAS1 specific for the human eosinophil derived neurotoxin. The
CC   method can be used to treat airway diseases such as cystic fibrosis,
CC   asthma, chronic obstructive pulmonary disease, bronchitis and other
CC   airway diseases characterised by an inflammatory response. By
CC   eliminating adenosine from the antisense ON, its liberation upon
CC   antisense degradation is prevented, thereby preventing adenosine-
CC   induced bronchoconstriction in patients with hyper-reactive airways.
XX
SQ   Sequence 20 BP; 0 A; 8 C; 4 G; 8 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 gccctgctgctctttctgct 20


RESULT   2
X53926
ID   X53926 standard; DNA; 20 BP.
XX
AC   X53926;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Eosinophil derived neurotoxin antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 46; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (X52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences X55272-74. These multiple target
CC   oligonucleotides (specifically X55180-271) can be used for the antisense
CC   treatment of diseases and conditions. Typical diseases and conditions
CC   are those associated with impaired respiration and inflammation,
CC   including lung diseases, pulmonary vasoconstriction, inflammation,
CC   allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC   respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC   hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC   carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC   cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC   metastases, as well as all types of cancers which may metastasize or have
CC   metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 20 BP; 0 A; 8 C; 4 G; 8 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 20;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 gccctgctgctctttctgct 20


RESULT   3
F19488
ID   F19488 standard; DNA; 20 BP.
XX
AC   F19488;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human eosinophil derived neurotoxin polynucleotide fragment #1055.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Claim 14; Page 142; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
```

CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 20 BP; 0 A; 8 C; 4 G; 8 T; 0 other;

```
  Query Match             100.0%;  Score 20;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 gccctgctgctctttctgct 20
```

RESULT 4
A33366
ID A33366 standard; DNA; 20 BP.
XX
AC A33366;
XX
DT 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:1055.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Claim 18; Page 397; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
SQ Sequence 20 BP; 0 A; 8 C; 4 G; 8 T; 0 other;

```
  Query Match             100.0%;  Score 20;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 gccctgctgctctttctgct 20
```

RESULT 5
X54599
ID X54599 standard; DNA; 156 BP.
XX
AC X54599;
XX
DT 05-JUL-1999 (first entry)
XX
DE Eosinophil derived neurotoxin antisense oligonucleotide fragment.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX

```
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 46; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (X52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences X55272-74. These multiple target
CC   oligonucleotides (specifically X55180-271) can be used for the antisense
CC   treatment of diseases and conditions. Typical diseases and conditions
CC   are those associated with impaired respiration and inflammation,
CC   including lung diseases, pulmonary vasoconstriction, inflammation,
CC   allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC   respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC   hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC   carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC   cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC   metastases, as well as all types of cancers which may metastasize or have
CC   metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 156 BP; 0 A; 41 C; 44 G; 51 T; 20 other;


  Query Match             100.0%;  Score 20;  DB 20;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 9.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 gccctgctgctctttctgct 20


RESULT   6
F20168
ID   F20168 standard; DNA; 156 BP.
XX
AC   F20168;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human eosinophil derived neurotoxin polynucleotide fragment #1735.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Claim 14; Page 142; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC   and antisense oligonucleotides used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 156 BP; 0 A; 41 C; 44 G; 51 T; 20 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 9.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 gccctgctgctctttctgct 20


RESULT   7
A34046
ID   A34046 standard; DNA; 156 BP.
XX
AC   A34046;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:1735.
```

```
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Disclosure; Page 480; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. A32313 to A35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC   to A33992) are specifically claimed ONs from the present invention.
CC   N.B. Sequences given in the disclosure of the present invention do not
CC   match up with their corresponding SEQ ID NO: sequences given in the
CC   sequence listing.
XX
SQ   Sequence 156 BP; 0 A; 41 C; 44 G; 51 T; 20 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 9.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 gccctgctgctctttctgct 20


RESULT   8
F21295/c
ID   F21295 standard; DNA; 1452 BP.
XX
AC   F21295;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human low adenosine antisense oligonucleotide related sequence #2862.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Disclosure; Page 1288-1289; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC   and antisense oligonucleotides used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 1452 BP; 380 A; 376 C; 323 G; 373 T; 0 other;
```

```
  Query Match             100.0%;  Score 20;  DB 21;  Length 1452;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCCCTGCTGCTCTTTCTGCT 20
           ||||||||||||||||||||
Db     110 GCCCTGCTGCTCTTTCTGCT 91


RESULT   9
A35173/c
ID   A35173 standard; DNA; 1452 BP.
XX
AC   A35173;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide 2nd SEQ ID NO:47.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Disclosure; Page 1205-1206; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. A32313 to A35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC   to A33992) are specifically claimed ONs from the present invention.
CC   N.B. Sequences given in the disclosure of the present invention do not
CC   match up with their corresponding SEQ ID NO: sequences given in the
CC   sequence listing.
XX
SQ   Sequence 1452 BP; 380 A; 376 C; 323 G; 373 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 1452;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCCCTGCTGCTCTTTCTGCT 20
           ||||||||||||||||||||
Db     110 GCCCTGCTGCTCTTTCTGCT 91


RESULT  10
F21298/c
ID   F21298 standard; DNA; 1489 BP.
XX
AC   F21298;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human low adenosine antisense oligonucleotide related sequence #2865.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Disclosure; Page 1290; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
```

CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 1489 BP; 411 A; 381 C; 320 G; 377 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 1489;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCTGCTGCTCTTTCTGCT 20
||||||||||||||||||||
Db 110 GCCCTGCTGCTCTTTCTGCT 91

RESULT 11
A35176/c
ID A35176 standard; DNA; 1489 BP.
XX
AC A35176;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:50.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 1207; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
SQ Sequence 1489 BP; 411 A; 381 C; 320 G; 377 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 1489;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCTGCTGCTCTTTCTGCT 20
||||||||||||||||||||
Db 110 GCCCTGCTGCTCTTTCTGCT 91

RESULT 12
F21296/c
ID F21296 standard; DNA; 2885 BP.
XX
AC F21296;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2863.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;

```
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Disclosure; Page 1289; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC   and antisense oligonucleotides used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 2885 BP; 752 A; 772 C; 608 G; 753 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 2885;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCCCTGCTGCTCTTTCTGCT 20
           ||||||||||||||||||||
Db    1543 GCCCTGCTGCTCTTTCTGCT 1524


RESULT  13
A35174/c
ID   A35174 standard; DNA; 2885 BP.
XX
AC   A35174;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide 2nd SEQ ID NO:48.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Disclosure; Page 1206; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. A32313 to A35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC   to A33992) are specifically claimed ONs from the present invention.
CC   N.B. Sequences given in the disclosure of the present invention do not
CC   match up with their corresponding SEQ ID NO: sequences given in the
CC   sequence listing.
XX
SQ   Sequence 2885 BP; 752 A; 772 C; 608 G; 753 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 2885;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCCCTGCTGCTCTTTCTGCT 20
           ||||||||||||||||||||
Db    1543 GCCCTGCTGCTCTTTCTGCT 1524


RESULT  14
F21300/c
ID   F21300 standard; DNA; 2918 BP.
XX
AC   F21300;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human low adenosine antisense oligonucleotide related sequence #2867.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
```

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 1291; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 2918 BP; 815 A; 786 C; 569 G; 748 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 2918;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCTGCTGCTCTTTCTGCT 20
||||||||||||||||||||
Db 804 GCCCTGCTGCTCTTTCTGCT 785

RESULT 15
A35178/c

ID A35178 standard; DNA; 2918 BP.
XX
AC A35178;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:52.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 1208; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
SQ Sequence 2918 BP; 815 A; 786 C; 569 G; 748 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 2918;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 GCCCTGCTGCTCTTTCTGCT 20
           ||||||||||||||||||||
Db     804 GCCCTGCTGCTCTTTCTGCT 785
```

Search completed: April 20, 2001, 00:13:00
Job time: 10022 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:25:00 ; Search time 7150.85 Seconds
(without alignments)
0.409 Million cell updates/sec

Title: US-09-016-464-19
Perfect score: 20
Sequence: 1 GCCCTGCTGCTCTTTCTGCT 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	18.4	92.0	827	143	BF065220	BF065220 HV_CEb002
2	17.4	87.0	239	119	AW725116	AW725116 f9h03nm.f
3	17.4	87.0	317	173	BG091258	BG091258 mac22a01.
4	17.4	87.0	355	30	AV606933	AV606933 AV606933
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7	17.4	87.0	366	119	AW717816	AW717816 i1f04nm.f
8	17.4	87.0	366	119	AW717817	AW717817 i1f04nm.f
9	17.4	87.0	367	119	AW723576	AW723576 e8h03nm.f
10	17.4	87.0	367	119	AW724066	AW724066 f3f06nm.f
11	17.4	87.0	404	119	AW716907	AW716907 h5e04nm.f
12	17.4	87.0	419	18	AI321994	AI321994 e6d01nm.f
13	17.4	87.0	421	18	AI321511	AI321511 d8h04nm.f
14	17.4	87.0	426	119	AW724312	AW724312 f4h06nm.f
15	17.4	87.0	429	119	AW716525	AW716525 h2h03nm.f
16	17.4	87.0	429	119	AW724574	AW724574 f6f06nm.f
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	22	17.4	87.0	451	15	AI021580	AI021580 ub13c10.r
	23	17.4	87.0	460	18	AI318817	AI318817 a2e08nm.f
	24	17.4	87.0	460	20	AI407401	AI407401 EST235690
c	25	17.4	87.0	463	22	AI594063	AI594063 vo77d07.y
	26	17.4	87.0	473	18	AI318698	AI318698 a1a04nm.f
c	27	17.4	87.0	478	18	AI294680	AI294680 LP08109.5
c	28	17.4	87.0	480	223	AZ506583	AZ506583 1M0347L15
	29	17.4	87.0	490	119	AW724800	AW724800 f8c06nm.f
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	34	17.4	87.0	520	206	AQ404731	AQ404731 HS_5048_A
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	37	17.4	87.0	535	122	AW941497	AW941497 LD02310.3
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	40	17.4	87.0	543	30	AV432475	AV432475 AV432475
	41	17.4	87.0	544	30	AV434870	AV434870 AV434870
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c	43	17.4	87.0	586	162	BE061063	BE061063 QV0-BT004
c	44	17.4	87.0	613	148	BF467953	BF467953 UI-M-CC0-
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ALIGNMENTS

```
RESULT   1
BF065220/c
LOCUS       BF065220      827 bp    mRNA            EST       17-OCT-2000
DEFINITION  HV_CEb0024E19f Hordeum vulgare seedling green leaf EST library
            HVcDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
            HV_CEb0024E19f, mRNA sequence.
ACCESSION   BF065220
VERSION     BF065220.1  GI:10841859
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
            Hordeum.
REFERENCE   1  (bases 1 to 827)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
            ,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
            Wood,T.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence start: 2
            High quality sequence stop: 644.
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                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1"
BASE COUNT      166 a    268 c    265 g    128 t
ORIGIN


  Query Match             92.0%;  Score 18.4;  DB 143;  Length 827;
  Best Local Similarity   95.0%;  Pred. No. 5.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          |||||||||||| ||||||||
Db    657 GCCCTGCTGCTGTTTCTGCT 638


RESULT   2
AW725116
LOCUS       AW725116      239 bp    mRNA            EST       19-APR-2000
DEFINITION  f9h03nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
            cDNA clone f9h03nm 5', mRNA sequence.
ACCESSION   AW725116
VERSION     AW725116.1  GI:7619676
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 239)
  AUTHORS   Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
  TITLE     Two Neurospora crassa EST Databases
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 208.
FEATURES             Location/Qualifiers
     source          1. .239
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                     /db_xref="taxon:5141"
                     /clone="f9h03nm"
                     /clone_lib="Neurospora crassa morning cDNA library"
                     /tissue_type="tissue harvested following 22hr growth in
                     dark"
                     /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
                     EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
                     5' end of cDNA cloned into XbaI site of pBluescript; 3'
                     end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT       74 a     79 c     28 g     58 t
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 119;  Length 239;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
          | ||||||||||||||||||
Db    214 CACTGCTGCTCTTTCTGCT 232


RESULT   3
BG091258
LOCUS       BG091258      317 bp    mRNA            EST       26-JAN-2001
DEFINITION  mac22a01.y1 Soares mouse 3NbMS Mus musculus cDNA clone
            IMAGE:4000393 5', mRNA sequence.
```

```
ACCESSION   BG091258
VERSION     BG091258.1  GI:12573821
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 317)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1498121
            Seq primer: -40RP from Gibco
            High quality sequence stop: 310.
FEATURES             Location/Qualifiers
     source          1. .317
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4000393"
                     /clone_lib="Soares mouse 3NbMS"
                     /sex="male"
                     /tissue_type="Spleen"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTGTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through
                     three rounds of normalization, and was constructed by
                     Bento Soares and M.Fatima Bonaldo."
BASE COUNT       70 a    100 c     58 g     89 t
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 173;  Length 317;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
          ||||||| ||||||||||
Db    245 CCCTGCTTCTCTTTCTGCT 263


RESULT   4
AV606933
LOCUS       AV606933      355 bp    mRNA            EST       30-AUG-2000
DEFINITION  AV606933 Bos taurus kidney fetus Bos taurus cDNA clone E1KI037G08
            5', mRNA sequence.
ACCESSION   AV606933
VERSION     AV606933.1  GI:9737306
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 355)
  AUTHORS   Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitohzono,A. and
            Suzuki,H.
  TITLE     bovine cDNA sequencing
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshikazu Sugimoto
            Animal Genetics Division
            Shirakawa Institute of Animal Genetics
            Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
            Tel: 81-248-25-5641
            Fax: 81-248-25-5725
            Email: kazusugi@cocoa.ocn.ne.jp
            Single pass sequencing.
            This clone was obtained from a polyA-deleted cDNA library.
FEATURES             Location/Qualifiers
     source          1. .355
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone="E1KI037G08"
                     /clone_lib="Bos taurus kidney fetus"
                     /tissue_type="kidney"
                     /dev_stage="fetus"
                     /lab_host="DH10B"
                     /note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
                     was deleted from a Not1 site"
BASE COUNT       53 a    124 c     72 g    105 t      1 others
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 30;  Length 355;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||
Db     71 CCCTGCTGCTCTTTCTGGT 89


RESULT   5
BF603899/c
LOCUS       BF603899      355 bp    mRNA            EST       13-DEC-2000
DEFINITION  269522 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BF603899
VERSION     BF603899.1  GI:11701973
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 355)
  AUTHORS   Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
            Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
            ,W.W. and Keele,J.W.
  TITLE     Design and use of four pooled tissue normalized cDNA libraries for
            EST discovery in cattle
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 50  row: B  column: 5
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .355
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 3BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
```

Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
BASE COUNT 101 a 76 c 69 g 109 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 150; Length 355;
Best Local Similarity 94.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGCTGCTCTTTCTGCT 20
||||||||||||| |||||
Db 54 CCCTGCTGCTCTTGCTGCT 36

RESULT 6
AW723785
LOCUS AW723785 365 bp mRNA EST 19-APR-2000
DEFINITION f1c12nm.f1 Neurospora crassa morning cDNA library Neurospora crassa cDNA clone f1c12nm 5', mRNA sequence.
ACCESSION AW723785
VERSION AW723785.1 GI:7618345
KEYWORDS EST.
SOURCE Neurospora crassa.
ORGANISM Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
REFERENCE 1 (bases 1 to 365)
AUTHORS Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
TITLE Two Neurospora crassa EST Databases
JOURNAL Unpublished (1998)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 337.
FEATURES Location/Qualifiers
source 1. .365
/organism="Neurospora crassa"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="f1c12nm"
/clone_lib="Neurospora crassa morning cDNA library"
/tissue_type="tissue harvested following 22hr growth in dark"
/note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2: EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996. 5' end of cDNA cloned into XbaI site of pBluescript; 3' end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT 92 a 120 c 59 g 94 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 119; Length 365;
Best Local Similarity 94.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGCTGCTCTTTCTGCT 20
| |||||||||||||||||
Db 214 CACTGCTGCTCTTTCTGCT 232

RESULT 7
AW717816
LOCUS AW717816 366 bp mRNA EST 19-APR-2000
DEFINITION i1f04nm.f1 Neurospora crassa morning cDNA library Neurospora crassa cDNA clone i1f04nm 5', mRNA sequence.
ACCESSION AW717816
VERSION AW717816.1 GI:7607061
KEYWORDS EST.
SOURCE Neurospora crassa.
ORGANISM Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
REFERENCE 1 (bases 1 to 366)
AUTHORS Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
TITLE Two Neurospora crassa EST Databases
JOURNAL Unpublished (1998)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 333.
FEATURES Location/Qualifiers
source 1. .366
/organism="Neurospora crassa"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="i1f04nm"
/clone_lib="Neurospora crassa morning cDNA library"
/tissue_type="tissue harvested following 22hr growth in dark"
/note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2: EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996. 5' end of cDNA cloned into XbaI site of pBluescript; 3' end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT 92 a 120 c 60 g 94 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 119; Length 366;
Best Local Similarity 94.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGCTGCTCTTTCTGCT 20
| |||||||||||||||||
Db 214 CACTGCTGCTCTTTCTGCT 232

RESULT 8
AW717817
LOCUS AW717817 366 bp mRNA EST 19-APR-2000
DEFINITION i1f04nm.f2 Neurospora crassa morning cDNA library Neurospora crassa cDNA clone i1f04nm 5', mRNA sequence.
ACCESSION AW717817
VERSION AW717817.1 GI:7607062
KEYWORDS EST.
SOURCE Neurospora crassa.
ORGANISM Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
REFERENCE 1 (bases 1 to 366)
AUTHORS Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
TITLE Two Neurospora crassa EST Databases
JOURNAL Unpublished (1998)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal

```
           Genetics Stock Center
           Seq primer: Universal Forward Primer
           High quality sequence stop: 333.
FEATURES             Location/Qualifiers
     source          1. .366
                     /organism="Neurospora crassa"
                     /strain="bd, frq7 A"
                     /db_xref="taxon:5141"
                     /clone="i1f04nm"
                     /clone_lib="Neurospora crassa morning cDNA library"
                     /tissue_type="tissue harvested following 22hr growth in
                     dark"
                     /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
                     EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
                     5' end of cDNA cloned into XbaI site of pBluescript; 3'
                     end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT       92 a    120 c     60 g     94 t
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 119;  Length 366;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCCTGCTGCTCTTTCTGCT 20
           | ||||||||||||||||||
Db     214 CACTGCTGCTCTTTCTGCT 232


RESULT   9
AW723576
LOCUS       AW723576      367 bp    mRNA            EST       19-APR-2000
DEFINITION  e8h03nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
            cDNA clone e8h03nm 5', mRNA sequence.
ACCESSION   AW723576
VERSION     AW723576.1  GI:7618136
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 367)
  AUTHORS   Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
  TITLE     Two Neurospora crassa EST Databases
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 338.
FEATURES             Location/Qualifiers
     source          1. .367
                     /organism="Neurospora crassa"
                     /strain="bd, frq7 A"
                     /db_xref="taxon:5141"
                     /clone="e8h03nm"
                     /clone_lib="Neurospora crassa morning cDNA library"
                     /tissue_type="tissue harvested following 22hr growth in
                     dark"
                     /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
                     EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
                     5' end of cDNA cloned into XbaI site of pBluescript; 3'
                     end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT       92 a    121 c     60 g     94 t
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 119;  Length 367;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCCTGCTGCTCTTTCTGCT 20
           | ||||||||||||||||||
Db     214 CACTGCTGCTCTTTCTGCT 232


RESULT  10
AW724066
LOCUS       AW724066      367 bp    mRNA            EST       19-APR-2000
DEFINITION  f3f06nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
            cDNA clone f3f06nm 5', mRNA sequence.
ACCESSION   AW724066
VERSION     AW724066.1  GI:7618626
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 367)
  AUTHORS   Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
  TITLE     Two Neurospora crassa EST Databases
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 251.
FEATURES             Location/Qualifiers
     source          1. .367
                     /organism="Neurospora crassa"
                     /strain="bd, frq7 A"
                     /db_xref="taxon:5141"
                     /clone="f3f06nm"
                     /clone_lib="Neurospora crassa morning cDNA library"
                     /tissue_type="tissue harvested following 22hr growth in
                     dark"
                     /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
                     EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
                     5' end of cDNA cloned into XbaI site of pBluescript; 3'
                     end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT       92 a    121 c     60 g     94 t
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 119;  Length 367;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCCTGCTGCTCTTTCTGCT 20
           | ||||||||||||||||||
Db     214 CACTGCTGCTCTTTCTGCT 232


RESULT  11
AW716907
LOCUS       AW716907      404 bp    mRNA            EST       19-APR-2000
DEFINITION  h5e04nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
            cDNA clone h5e04nm 5', mRNA sequence.
ACCESSION   AW716907
VERSION     AW716907.1  GI:7606132
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
```

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            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 404)
  AUTHORS   Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
  TITLE     Two Neurospora crassa EST Databases
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 184.
FEATURES             Location/Qualifiers
     source          1. .404
                     /organism="Neurospora crassa"
                     /strain="bd, frq7 A"
                     /db_xref="taxon:5141"
                     /clone="h5e04nm"
                     /clone_lib="Neurospora crassa morning cDNA library"
                     /tissue_type="tissue harvested following 22hr growth in
                     dark"
                     /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
                     EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
                     5' end of cDNA cloned into XbaI site of pBluescript; 3'
                     end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT      104 a    128 c     67 g    105 t
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 119;  Length 404;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
          | ||||||||||||||||||
Db    214 CACTGCTGCTCTTTCTGCT 232


RESULT  12
AI321994
LOCUS       AI321994      419 bp    mRNA            EST       18-DEC-1998
DEFINITION  e6d01nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
            cDNA clone e6d01nm 5', mRNA sequence.
ACCESSION   AI321994
VERSION     AI321994.1  GI:4037976
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 419)
  AUTHORS   Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
  TITLE     Two Neurospora crassa EST Databases
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 279.
FEATURES             Location/Qualifiers
     source          1. .419
                     /organism="Neurospora crassa"
                     /strain="bd, frq7 A"
                     /db_xref="taxon:5141"
                     /clone="e6d01nm"
                     /clone_lib="Neurospora crassa morning cDNA library"
                     /tissue_type="tissue harvested following 22hr growth in
                     dark"
                     /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
                     EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
                     5' end of cDNA cloned into XbaI site of pBluescript; 3'
                     end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT      107 a    135 c     69 g    108 t
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 18;  Length 419;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
          | ||||||||||||||||||
Db    214 CACTGCTGCTCTTTCTGCT 232


RESULT  13
AI321511
LOCUS       AI321511      421 bp    mRNA            EST       18-DEC-1998
DEFINITION  d8h04nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
            cDNA clone d8h04nm 5', mRNA sequence.
ACCESSION   AI321511
VERSION     AI321511.1  GI:4037493
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 421)
  AUTHORS   Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
  TITLE     Two Neurospora crassa EST Databases
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 337.
FEATURES             Location/Qualifiers
     source          1. .421
                     /organism="Neurospora crassa"
                     /strain="bd, frq7 A"
                     /db_xref="taxon:5141"
                     /clone="d8h04nm"
                     /clone_lib="Neurospora crassa morning cDNA library"
                     /tissue_type="tissue harvested following 22hr growth in
                     dark"
                     /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
                     EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
                     5' end of cDNA cloned into XbaI site of pBluescript; 3'
                     end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT      107 a    131 c     70 g    109 t      4 others
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 18;  Length 421;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
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Db    213 CACTGCTGCTCTTTCTGCT 231
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RESULT  14
AW724312
LOCUS       AW724312      426 bp    mRNA            EST       19-APR-2000
DEFINITION  f4h06nm.f2 Neurospora crassa morning cDNA library Neurospora crassa
            cDNA clone f4h06nm 5', mRNA sequence.
ACCESSION   AW724312
VERSION     AW724312.1  GI:7618872
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
  TITLE     Two Neurospora crassa EST Databases
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 347.
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Neurospora crassa"
                     /strain="bd, frq7 A"
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                     /clone="f4h06nm"
                     /clone_lib="Neurospora crassa morning cDNA library"
                     /tissue_type="tissue harvested following 22hr growth in
                     dark"
                     /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
                     EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
                     5' end of cDNA cloned into XbaI site of pBluescript; 3'
                     end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT      109 a    138 c     70 g    109 t
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 119;  Length 426;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
          | ||||||||||||||||||
Db    214 CACTGCTGCTCTTTCTGCT 232


RESULT  15
AW716525
LOCUS       AW716525      429 bp    mRNA            EST       19-APR-2000
DEFINITION  h2h03nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
            cDNA clone h2h03nm 5', mRNA sequence.
ACCESSION   AW716525
VERSION     AW716525.1  GI:7605743
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 429)
  AUTHORS   Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
  TITLE     Two Neurospora crassa EST Databases
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 228.
FEATURES             Location/Qualifiers
     source          1. .429
                     /organism="Neurospora crassa"
                     /strain="bd, frq7 A"
                     /db_xref="taxon:5141"
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                     /clone_lib="Neurospora crassa morning cDNA library"
                     /tissue_type="tissue harvested following 22hr growth in
                     dark"
                     /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
                     EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
                     5' end of cDNA cloned into XbaI site of pBluescript; 3'
                     end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT      109 a    140 c     70 g    110 t
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 119;  Length 429;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
          | ||||||||||||||||||
Db    214 CACTGCTGCTCTTTCTGCT 232


Search completed: April 19, 2001, 23:25:03
Job time: 8180 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:03:45 ; Search time 280.46 Seconds
(without alignments)
12.451 Million cell updates/sec

Title: US-09-016-464-19
Perfect score: 20
Sequence: 1 GCCCTGCTGCTCTTTCTGCT 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	16.8	84.0	24979	2	US-08-147-777-3	Sequence 3, Appli
3	16.8	84.0	24979	3	US-08-452-872-3	Sequence 3, Appli
4	16.8	84.0	24979	5	PCT-US93-03985-3	Sequence 3, Appli
c 5	16.4	82.0	2290	4	US-08-961-083-65	Sequence 65, Appl
c 6	16.4	82.0	5816	4	US-09-220-641-4	Sequence 4, Appli
c 7	15.8	79.0	441	2	US-08-975-316-60	Sequence 60, Appl
c 8	15.8	79.0	1272	3	US-08-952-664-9	Sequence 9, Appli
c 9	15.8	79.0	1680	1	US-08-234-783-3	Sequence 3, Appli
c 10	15.8	79.0	1680	1	US-08-456-907-3	Sequence 3, Appli
c 11	15.8	79.0	1680	5	PCT-US95-05523-3	Sequence 3, Appli
12	15.8	79.0	1809	1	US-08-453-956-24	Sequence 24, Appl
13	15.8	79.0	1809	1	US-08-086-631-24	Sequence 24, Appl
14	15.8	79.0	1809	2	US-08-452-930-24	Sequence 24, Appl
15	15.8	79.0	1809	5	PCT-US93-08174-24	Sequence 24, Appl
c 16	15.4	77.0	94	1	US-08-123-343A-3	Sequence 3, Appli
c 17	15.4	77.0	372	2	US-08-822-573-1	Sequence 1, Appli
c 18	15.4	77.0	798	1	US-08-123-343A-1	Sequence 1, Appli
c 19	15.4	77.0	1080	1	US-07-954-840A-11	Sequence 11, Appl
c 20	15.4	77.0	1080	1	US-07-954-840A-17	Sequence 17, Appl
c 21	15.4	77.0	1799	2	US-08-453-848-10	Sequence 10, Appl
c 22	15.4	77.0	2201	4	US-09-330-970-2	Sequence 2, Appli
23	15.4	77.0	2242	3	US-09-400-742-1	Sequence 1, Appli
24	15.4	77.0	2242	4	US-08-618-651A-1	Sequence 1, Appli
c 25	15.4	77.0	3336	4	US-09-330-970-4	Sequence 4, Appli
c 26	15.4	77.0	3611	2	US-08-727-118-1	Sequence 1, Appli
c 27	15.4	77.0	6306	1	US-08-466-390-3	Sequence 3, Appli
c 28	15.4	77.0	6306	1	US-08-470-950-3	Sequence 3, Appli
c 29	15.4	77.0	6306	1	US-08-467-781-3	Sequence 3, Appli
c 30	15.4	77.0	6306	1	US-08-195-487-3	Sequence 3, Appli
c 31	15.4	77.0	6306	2	US-08-483-924-3	Sequence 3, Appli
c 32	15.4	77.0	6306	5	PCT-US93-06160-3	Sequence 3, Appli
33	15.2	76.0	105	2	US-08-476-176B-19	Sequence 19, Appl
34	15.2	76.0	105	3	US-08-127-721A-19	Sequence 19, Appl
35	15.2	76.0	105	3	US-08-485-246A-19	Sequence 19, Appl
c 36	15.2	76.0	286	2	US-08-332-766A-6	Sequence 6, Appli
37	15.2	76.0	378	3	US-07-765-830A-3	Sequence 3, Appli
38	15.2	76.0	378	3	US-07-765-830A-8	Sequence 8, Appli
39	15.2	76.0	424	2	US-08-476-176B-5	Sequence 5, Appli
40	15.2	76.0	424	2	US-08-476-176B-7	Sequence 7, Appli
41	15.2	76.0	424	2	US-08-476-176B-9	Sequence 9, Appli
42	15.2	76.0	424	3	US-08-127-721A-5	Sequence 5, Appli
43	15.2	76.0	424	3	US-08-127-721A-7	Sequence 7, Appli
44	15.2	76.0	424	3	US-08-127-721A-9	Sequence 9, Appli
45	15.2	76.0	424	3	US-08-485-246A-5	Sequence 5, Appli

ALIGNMENTS

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RESULT   1
US-07-662-005A-15/c
; Sequence 15, Application US/07662005A
; Patent No. 5246838
;  GENERAL INFORMATION:
;    APPLICANT:  Van Dijl, Jan M.
;    APPLICANT:  Smith, Hilde E.
;    APPLICANT:  Bron, Sierd
;    APPLICANT:  Quax, Wilhelmus J.
;    TITLE OF INVENTION:  IMPROVED PROCESSING OF PROTEINS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/662,005A
;      FILING DATE:  19910228
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  246152002300
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-813-5600
;      TELEFAX:  415-494-0792
;      TELEX:  34-0154
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1314 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-662-005A-15


  Query Match             100.0%;  Score 20;  DB 1;  Length 1314;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
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Qy       1 GCCCTGCTGCTCTTTCTGCT 20
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Db    110 GCCCTGCTGCTCTTTCTGCT 91


RESULT   2
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; Sequence 3, Application US/08147777
; Patent No. 5914265
;  GENERAL INFORMATION:
;    APPLICANT:  Roop, Dennis R.
;    APPLICANT:  Rothnagel, Joseph A.
;    APPLICANT:  Greenhalgh, David A.
;    APPLICANT:  Yuspa, Stuart H.
;    TITLE OF INVENTION:  KERATIN K1 EXPRESSION VECTORS
;    TITLE OF INVENTION:  AND METHODS OF USE
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LYON & LYON
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  IBM MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/147,777
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:              two
;      APPLICATION NUMBER:  07/876,289
;      FILING DATE:  April 30, 1992
;      APPLICATION NUMBER:  Unassigned (204/144)
;      FILING DATE:  October 29, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  204/153
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24979 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-147-777-3


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  Best Local Similarity   90.0%;  Pred. No. 76;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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RESULT   3
US-08-452-872-3
; Sequence 3, Application US/08452872
; Patent No. 6057298
;  GENERAL INFORMATION:
;    APPLICANT:  Roop, Dennis R.
;    APPLICANT:  Rothnagel, Joseph A.
;    APPLICANT:  Greenhalgh, David A.
;    APPLICANT:  Yuspa, Stuart H.
;    TITLE OF INVENTION:  KERATIN K1 EXPRESSION VECTORS
;    TITLE OF INVENTION:  AND METHODS OF USE
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LYON & LYON
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  IBM MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/452,872
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/147,777
;      FILING DATE:
;      APPLICATION NUMBER:  07/876,289
;      FILING DATE:  April 30, 1992
;      APPLICATION NUMBER:  Unassigned (204/144)
;      FILING DATE:  October 29, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  204/153
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24979 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-452-872-3


  Query Match             84.0%;  Score 16.8;  DB 3;  Length 24979;
  Best Local Similarity   90.0%;  Pred. No. 76;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          |||||||||||  || |||||
Db   5578 GCCCTGCTGCTGTTCCTGCT 5597


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PCT-US93-03985-3
; Sequence 3, Application PC/TUS9303985
;  GENERAL INFORMATION:
;    APPLICANT:  Roop, Dennis R.
;    APPLICANT:  Rothnagel, Joseph A.
;    APPLICANT:  Greenhalgh, David A.
;    APPLICANT:  Yuspa, Stuart H.
;    TITLE OF INVENTION:  DEVELOPMENT OF A VECTOR TO TARGET GENE
;    TITLE OF INVENTION:  EXPRESSION TO THE EPIDERMIS OF TRANSGENIC ANIMALS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/03985
;      FILING DATE:  19930428
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5478
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;      TELEX:  762829
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24979 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US93-03985-3


  Query Match             84.0%;  Score 16.8;  DB 5;  Length 24979;
  Best Local Similarity   90.0%;  Pred. No. 76;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          |||||||||||  || |||||
Db   5578 GCCCTGCTGCTGTTCCTGCT 5597


RESULT   5
US-08-961-083-65/c
; Sequence 65, Application US/08961083
; Patent No. 6159469
;  GENERAL INFORMATION:
;    APPLICANT:  Choi et. al.
;    TITLE OF INVENTION:  Streptococcus pneumoniae Antigens and Vaccines
;    NUMBER OF SEQUENCES:  452
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/961,083
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brookes, A. Anders
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB340P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2290 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-961-083-65


  Query Match             82.0%;  Score 16.4;  DB 4;  Length 2290;
  Best Local Similarity   94.4%;  Pred. No. 89;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 CCTGCTGCTCTTTCTGCT 20
          |||||||| ||||||||
Db   1203 CCTGCTGCTGTTTCTGCT 1186


RESULT   6
US-09-220-641-4/c
; Sequence 4, Application US/09220641
; Patent No. 6210923
; GENERAL INFORMATION:
;  APPLICANT: Lee, Cheng-Chi
;  APPLICANT: Sun, Zhong Sheng
;  APPLICANT: Albrecht, Urs
;  APPLICANT: Eichele, Gregor
;  TITLE OF INVENTION: Mammalian Circadian Regulator M-RIGUI2 (M-PER2)
;  FILE REFERENCE: D6067
;  CURRENT APPLICATION NUMBER: US/09/220,641
;  CURRENT FILING DATE: 1998-12-24
;  EARLIER APPLICATION NUMBER: US 60/068,886
;  EARLIER FILING DATE: 1997-12-26
;  NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 4
;   LENGTH: 5816
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 145..3918
;   OTHER INFORMATION: m-rigui2 cDNA Sequence
US-09-220-641-4


  Query Match             82.0%;  Score 16.4;  DB 4;  Length 5816;
  Best Local Similarity   94.4%;  Pred. No. 97;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTG 18
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Db   2340 GCCCTGCTCCTCTTTCTG 2323


RESULT   7
US-08-975-316-60/c
; Sequence 60, Application US/08975316
; Patent No. 5952486
;  GENERAL INFORMATION:
;    APPLICANT:  BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
;    APPLICANT:  and GRIERSON, Alastair W.
;    TITLE OF INVENTION:  MATERIALS AND METHODS FOR
;    TITLE OF INVENTION:  THE MODIFICATION OF PLANT LIGNIN CONTENT
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Ann W. Speckman
;      STREET:  2601 Elliott Avenue, Suite 4185
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
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;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/975,316
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/713,000
;      FILING DATE:  September 11, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SLEATH, Janet
;      REGISTRATION NUMBER:  37,007
;      REFERENCE/DOCKET NUMBER:  11000/1003C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-269-0565
;      TELEFAX:  206-269-0563
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  441 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-975-316-60


  Query Match             79.0%;  Score 15.8;  DB 2;  Length 441;
  Best Local Similarity   89.5%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
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Db    404 CCATGCTGCTTTTTCTGCT 386


RESULT   8
US-08-952-664-9/c
; Sequence 9, Application US/08952664
; Patent No. 6034235
;  GENERAL INFORMATION:
;    APPLICANT:  SUGIYAMA, Haruo
;    APPLICANT:  YAMAGAMI, Tamotsu
;    APPLICANT:  INOUE, Kazushi
;    TITLE OF INVENTION:  GROWTH INHIBITOR FOR LEUKEMIA CELLS
;    TITLE OF INVENTION:  COMPRISING ANTISENSE OLIGONUCLEOTIDE DERIVATIVE TO WILMS
;    TITLE OF INVENTION:  TUMOR GENE (WT1)
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY & LARDNER
;      STREET:  3000 K Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/952,664
;      FILING DATE:  01-DEC-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP96/01394
;      FILING DATE:  24-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-156672
;      FILING DATE:  01-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wegner, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  053466/0223
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 672-5300
;      TELEFAX:  (202) 672-5399
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1272 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Synthetic DNA"
US-08-952-664-9


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  Best Local Similarity   89.5%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
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Db   1268 CCCTGCTGCTCTGGCTGCT 1250


RESULT   9
US-08-234-783-3/c
; Sequence 3, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1680 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  381..1670
US-08-234-783-3


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  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy      2 CCCTGCTGCTCTTTCTGCT 20
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Db    271 CCCTGCTGCTCTGGCTGCT 253


RESULT  10
US-08-456-907-3/c
; Sequence 3, Application US/08456907
; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/456,907
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1680 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  381..1670
US-08-456-907-3


  Query Match             79.0%;  Score 15.8;  DB 1;  Length 1680;
  Best Local Similarity   89.5%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
          ||||||||||||  |||||
Db    271 CCCTGCTGCTCTGGCTGCT 253


RESULT  11
PCT-US95-05523-3/c
; Sequence 3, Application PC/TUS9505523
;  GENERAL INFORMATION:
;    APPLICANT:  The Wistar Institute of Anatomy and Biology
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and
;    TITLE OF INVENTION:  Methods of Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05523
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1680 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  381..1670
PCT-US95-05523-3


  Query Match             79.0%;  Score 15.8;  DB 5;  Length 1680;
  Best Local Similarity   89.5%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
          ||||||||||||  |||||
Db    271 CCCTGCTGCTCTGGCTGCT 253


RESULT  12
US-08-453-956-24
; Sequence 24, Application US/08453956
; Patent No. 5770445
;  GENERAL INFORMATION:
;    APPLICANT:  Kindsvogel, Waylne R.
;    TITLE OF INVENTION:  GLUCAGON RECEPTORS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED AND BERRY
;      STREET:  6300 COLUMBIA CENTER
;      CITY:  SEATTLE
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  99104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,956
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  530
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/086,631
;      FILING DATE:  July 1, 1993
;      APPLICATION NUMBER:  US 07/938,331
;      FILING DATE:  28-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  990008.424C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1809 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  pLJ6'
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..1486
US-08-453-956-24


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  Best Local Similarity   89.5%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 CCCTGCTGCTCTTTCTGCT 20
           |||||||||| || |||||
Db      78 CCCTGCTGCTGTTGCTGCT 96


RESULT  13
US-08-086-631-24
; Sequence 24, Application US/08086631
; Patent No. 5776725
;  GENERAL INFORMATION:
;    APPLICANT:  Kindsvogel, Waylne R.
;    TITLE OF INVENTION:  GLUCAGON RECEPTORS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED AND BERRY
;      STREET:  6300 COLUMBIA CENTER
;      CITY:  SEATTLE
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  99104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/086,631
;      FILING DATE:  July 1, 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/938,331
;      FILING DATE:  28-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  990008.424C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1809 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  pLJ6'
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..1486
US-08-086-631-24


  Query Match             79.0%;  Score 15.8;  DB 1;  Length 1809;
  Best Local Similarity   89.5%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 CCCTGCTGCTCTTTCTGCT 20
           |||||||||| || |||||
Db      78 CCCTGCTGCTGTTGCTGCT 96


RESULT  14
US-08-452-930-24
; Sequence 24, Application US/08452930
; Patent No. 5919635
;  GENERAL INFORMATION:
;    APPLICANT:  Kindsvogel, Waylne R.
;    TITLE OF INVENTION:  GLUCAGON RECEPTORS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED AND BERRY
;      STREET:  6300 COLUMBIA CENTER
;      CITY:  SEATTLE
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  99104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/452,930
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/086,631
;      FILING DATE:  July 1, 1993
;      APPLICATION NUMBER:  US 07/938,331
;      FILING DATE:  28-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  990008.424C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1809 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  pLJ6'
;    FEATURE:
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;      NAME/KEY:  CDS
;      LOCATION:  53..1486
US-08-452-930-24


  Query Match            79.0%;  Score 15.8;  DB 2;  Length 1809;
  Best Local Similarity   89.5%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 CCCTGCTGCTCTTTCTGCT 20
           |||||||||| || |||||
Db      78 CCCTGCTGCTGTTGCTGCT 96


RESULT  15
PCT-US93-08174-24
; Sequence 24, Application PC/TUS9308174
;  GENERAL INFORMATION:
;    APPLICANT:
;    APPLICANT:  NAME: ZymoGynetics, Inc.
;    APPLICANT:  STREET: 4225 Roosevelt Way North East
;    APPLICANT:  CITY: Seattle, Washington
;    APPLICANT:  COUNTRY: United States
;    APPLICANT:  POSTAL CODE: 98105
;    APPLICANT:  TELEPHONE: (206) 547-80808
;    TITLE OF INVENTION:  GLUCAGON RECEPTORS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED AND BERRY
;      STREET:  6300 COLUMBIA CENTER
;      CITY:  SEATTLE
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  99104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08174
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;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/086,631
;      FILING DATE:  July 1, 1993
;      APPLICATION NUMBER:  US 07/938,331
;      FILING DATE:  28-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  990008.424C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1809 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  pLJ6'
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..1486
PCT-US93-08174-24


  Query Match            79.0%;  Score 15.8;  DB 5;  Length 1809;
  Best Local Similarity   89.5%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 CCCTGCTGCTCTTTCTGCT 20
           |||||||||| || |||||
Db      78 CCCTGCTGCTGTTGCTGCT 96


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GenCore version 4.5

OM nucleic - nucleic search, using sw model

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Title: US-09-016-464-19
Perfect score: 20
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Searched: 13168883 seqs, 2603265903 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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39: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
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45: /cgn2_6/ptodata/2/pna/US6013_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US6014_COMB.seq:*
47: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
48: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
49: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*
50: /cgn2_6/ptodata/2/pna/US6018_COMB.seq:*
51: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
52: /cgn2_6/ptodata/2/pna/US6020_COMB.seq:*
53: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:*
54: /cgn2_6/ptodata/2/pna/US6022_COMB.seq:*
55: /cgn2_6/ptodata/2/pna/US6023_COMB.seq:*
56: /cgn2_6/ptodata/2/pna/US6024_COMB.seq:*
57: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
58: /cgn2_6/ptodata/2/pna/US6026_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	8	US-08-474-497-19	Sequence 19, Appl
2		20	100.0	20	14	US-09-016-464-19	Sequence 19, Appl
3		20	100.0	20	19	US-09-509-152A-1055	Sequence 1055, Ap
4		20	100.0	156	19	US-09-509-152A-1735	Sequence 1735, Ap
5	c	20	100.0	1278	8	US-08-430-121-17	Sequence 17, Appl
6	c	20	100.0	1310	8	US-08-430-121-18	Sequence 18, Appl
7	c	20	100.0	1314	8	US-08-430-121-16	Sequence 16, Appl
8	c	20	100.0	1493	17	US-09-359-922-10109	Sequence 10109, A
9	c	20	100.0	1493	17	US-09-359-922-10109	Sequence 10109, A
10		20	100.0	7033	19	US-09-509-152A-2411	Sequence 2411, Ap
11	c	18	90.0	118773	53	US-60-212-664-10	Sequence 10, Appl
12	c	18	90.0	118773	53	US-60-212-664-251	Sequence 251, App
13	c	18	90.0	118773	53	US-60-212-664-302	Sequence 302, App
14	c	17.4	87.0	50	53	US-60-217-080-9433	Sequence 9433, Ap
15		17.4	87.0	305	21	US-09-540-733-6246	Sequence 6246, Ap
16		17.4	87.0	305	26	US-09-668-683-10057	Sequence 10057, A
17		17.4	87.0	305	47	US-60-156-625-3251	Sequence 3251, Ap
18	c	17.4	87.0	782	29	US-09-739-449-1514	Sequence 1514, Ap
19	c	17.4	87.0	867	16	US-09-221-017B-791	Sequence 791, App
20	c	17.4	87.0	871	24	US-09-620-392-25784	Sequence 25784, A
21	c	17.4	87.0	871	28	US-09-702-134-38385	Sequence 38385, A
22	c	17.4	87.0	1125	16	US-09-270-767-13983	Sequence 13983, A
23		17.4	87.0	1478	51	US-60-195-534-14	Sequence 14, Appl
24	c	17.4	87.0	1937	48	US-60-167-217-8100	Sequence 8100, Ap
25	c	17.4	87.0	1937	49	US-60-173-464-6498	Sequence 6498, Ap
26	c	17.4	87.0	2679	51	US-60-191-637-8003	Sequence 8003, Ap
27	c	17.4	87.0	2679	51	US-60-191-681-6248	Sequence 6248, Ap
28	c	17.4	87.0	4868	48	US-60-167-217-8099	Sequence 8099, Ap
29	c	17.4	87.0	4868	49	US-60-173-464-6497	Sequence 6497, Ap
30	c	17.4	87.0	13632	51	US-60-191-637-8002	Sequence 8002, Ap
31	c	17.4	87.0	13632	51	US-60-191-681-6247	Sequence 6247, Ap
32		17.4	87.0	66484	19	US-09-528-237A-902	Sequence 902, App
33		17.4	87.0	257574	19	US-09-528-237A-1454	Sequence 1454, Ap
34		17	85.0	273	13	US-08-923-861-58	Sequence 58, Appl
35		17	85.0	273	20	US-09-539-813-27	Sequence 27, Appl
36		17	85.0	273	34	US-60-024-690-58	Sequence 58, Appl
37	c	17	85.0	296	25	US-09-654-617-384753	Sequence 384753,
38	c	17	85.0	296	27	US-09-684-016-384753	Sequence 384753,
39	c	17	85.0	368	19	US-09-528-409-83109	Sequence 83109, A
40		17	85.0	376	16	US-09-271-122-7842	Sequence 7842, Ap
41		17	85.0	376	28	US-09-713-841-7842	Sequence 7842, Ap
42		17	85.0	382	16	US-09-205-070-283	Sequence 283, App
43		17	85.0	382	16	US-09-271-122-7843	Sequence 7843, Ap
44		17	85.0	382	17	US-09-340-623-283	Sequence 283, App
45		17	85.0	382	28	US-09-713-841-7843	Sequence 7843, Ap

ALIGNMENTS

```
RESULT   1
US-08-474-497-19
; Sequence 19, Application US/08474497
;  GENERAL INFORMATION:
;    APPLICANT:  Nyce, Jonathan W.
;    TITLE OF INVENTION:  Method of Treatment of Lung Diseases
;    TITLE OF INVENTION:  Using Antisense Oligonucleotides
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  Post Office Drawer 34009
;      CITY:  Charlotte
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,497
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5218-32
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 881-3140
;      TELEFAX:  (919) 881-3175
;      TELEX:  575102
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-474-497-19


  Query Match             100.0%;  Score 20;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 GCCCTGCTGCTCTTTCTGCT 20


RESULT   2
US-09-016-464-19
; Sequence 19, Application US/09016464
;   GENERAL INFORMATION:
;        APPLICANT: Nyce, Jonathan W.
;        TITLE OF INVENTION: Method of Treatment of Lung Diseases
;                            Using Antisense Oligonucleotides
;        NUMBER OF SEQUENCES: 44
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Kenneth D. Sibley
;             STREET: Post Office Drawer 34009
;             CITY: Charlotte
;             STATE: NC
;             COUNTRY: USA
;             ZIP: 28234
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/016,464
;             FILING DATE: 30-Jan-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/474,497
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sibley, Kenneth D.
;             REGISTRATION NUMBER: 31,665
;             REFERENCE/DOCKET NUMBER: 5218-32
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (919) 881-3140
;             TELEFAX: (919) 881-3175
;             TELEX: 575102
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-016-464-19


  Query Match             100.0%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 GCCCTGCTGCTCTTTCTGCT 20


RESULT   3
US-09-509-152A-1055
; Sequence 1055, Application US/09509152A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, JONATHAN W.
;        TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
;                            FORMULATIONS, KITS & APPLICATIONS
;        NUMBER OF SEQUENCES: 2419
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 CLARKE DRIVE
;             CITY: CRANBURY
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/509,152A
;             FILING DATE: 17-Mar-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/059,160
;             FILING DATE: 1997-09-17
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-00991
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1055:
;        SEQUENCE CHARACTERISTICS:
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;            LENGTH: 20 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1055:
US-09-509-152A-1055


  Query Match             100.0%;  Score 20;  DB 19;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 GCCCTGCTGCTCTTTCTGCT 20


RESULT   4
US-09-509-152A-1735
; Sequence 1735, Application US/09509152A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, JONATHAN W.
;        TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
;                            FORMULATIONS, KITS & APPLICATIONS
;        NUMBER OF SEQUENCES: 2419
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 CLARKE DRIVE
;             CITY: CRANBURY
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/509,152A
;             FILING DATE: 17-Mar-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/059,160
;             FILING DATE: 1997-09-17
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-00991
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1735:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 156 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1735:
US-09-509-152A-1735


  Query Match             100.0%;  Score 20;  DB 19;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 GCCCTGCTGCTCTTTCTGCT 20


RESULT   5
US-08-430-121-17/c
; Sequence 17, Application US/08430121
;  GENERAL INFORMATION:
;    APPLICANT:  Simonsen, Christian C.
;    APPLICANT:  McGrogan, Michael
;    TITLE OF INVENTION:  Recombinant Products of an Eosinophilic
;    TITLE OF INVENTION:  Gene Family
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,121
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,859
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/630,976
;      FILING DATE:  19-DEC-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Shetka, Debra A.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  24842-20058.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-813-5600
;      TELEFAX:  415-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1278 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-430-121-17


  Query Match             100.0%;  Score 20;  DB 8;  Length 1278;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db    110 GCCCTGCTGCTCTTTCTGCT 91


RESULT   6
US-08-430-121-18/c
; Sequence 18, Application US/08430121
;  GENERAL INFORMATION:
;    APPLICANT:  Simonsen, Christian C.
;    APPLICANT:  McGrogan, Michael
;    TITLE OF INVENTION:  Recombinant Products of an Eosinophilic
;    TITLE OF INVENTION:  Gene Family
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/430,121
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/232,859
;       FILING DATE:
;       APPLICATION NUMBER:  US 07/630,976
;       FILING DATE:  19-DEC-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Shetka, Debra A.
;       REGISTRATION NUMBER:  33,208
;       REFERENCE/DOCKET NUMBER:  24842-20058.00
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-813-5600
;       TELEFAX:  415-494-0792
;       TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  18:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1310 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-430-121-18


  Query Match             100.0%;  Score 20;  DB 8;  Length 1310;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db    110 GCCCTGCTGCTCTTTCTGCT 91


RESULT   7
US-08-430-121-16/c
; Sequence 16, Application US/08430121
;  GENERAL INFORMATION:
;     APPLICANT:  Simonsen, Christian C.
;     APPLICANT:  McGrogan, Michael
;     TITLE OF INVENTION:  Recombinant Products of an Eosinophilic
;     TITLE OF INVENTION:  Gene Family
;     NUMBER OF SEQUENCES:  18
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Morrison & Foerster
;       STREET:  755 Page Mill Road
;       CITY:  Palo Alto
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94304-1018
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/430,121
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/232,859
;       FILING DATE:
;       APPLICATION NUMBER:  US 07/630,976
;       FILING DATE:  19-DEC-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Shetka, Debra A.
;       REGISTRATION NUMBER:  33,208
;       REFERENCE/DOCKET NUMBER:  24842-20058.00
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-813-5600
;       TELEFAX:  415-494-0792
;       TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1314 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-430-121-16


  Query Match             100.0%;  Score 20;  DB 8;  Length 1314;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db    110 GCCCTGCTGCTCTTTCTGCT 91


RESULT   8
US-09-359-922-10109/c
; Sequence 10109, Application US/09359922
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS cDNA
;  TITLE OF INVENTION: LIBRARIES
;  FILE REFERENCE: 20411-752CON1
;  CURRENT APPLICATION NUMBER: US/09/359,922
;  CURRENT FILING DATE: 1999-07-22
;  EARLIER APPLICATION NUMBER: US 09/205,155
;  EARLIER FILING DATE: 1998-12-03
;  NUMBER OF SEQ ID NOS: 13203
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10109
;   LENGTH: 1493
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-359-922-10109


  Query Match             100.0%;  Score 20;  DB 17;  Length 1493;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db    111 GCCCTGCTGCTCTTTCTGCT 92


RESULT   9
US-09-359-922-10109/c
; Sequence 10109, Application US/09359922A
; GENERAL INFORMATION:
;  APPLICANT: Leshkowitz, Dena
;  APPLICANT: Liu, Jin
;  TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS cDNA
;  TITLE OF INVENTION: LIBRARIES
;  FILE REFERENCE: 20411-752CON1
;  CURRENT APPLICATION NUMBER: US/09/359,922A
;  CURRENT FILING DATE: 1999-07-22
;  EARLIER APPLICATION NUMBER: US 09/205,155
;  EARLIER FILING DATE: 1998-12-03
;  EARLIER APPLICATION NUMBER: US 09/034,341
;  EARLIER FILING DATE: 1998-02-13
;  NUMBER OF SEQ ID NOS: 13203
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10109
;   LENGTH: 1493
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-359-922-10109
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  Query Match            100.0%;  Score 20;  DB 17;  Length 1493;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db    111 GCCCTGCTGCTCTTTCTGCT 92


RESULT  10
US-09-509-152A-2411
; Sequence 2411, Application US/09509152A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, JONATHAN W.
;        TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
;                            FORMULATIONS, KITS & APPLICATIONS
;        NUMBER OF SEQUENCES: 2419
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 CLARKE DRIVE
;             CITY: CRANBURY
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/509,152A
;             FILING DATE: 17-Mar-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/059,160
;             FILING DATE: 1997-09-17
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-00991
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2411:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 7033 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2411:
US-09-509-152A-2411


  Query Match            100.0%;  Score 20;  DB 19;  Length 7033;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db     82 GCCCTGCTGCTCTTTCTGCT 101


RESULT  11
US-60-212-664-10/c
; Sequence 10, Application US/60212664
; GENERAL INFORMATION:
;  APPLICANT:  Ladunga, Steve
;  APPLICANT:  Spier, Gene
;  APPLICANT:  Greenberg, Simon
;  APPLICANT:  Rabkin, Steven
;  APPLICANT:  Wang, Yu
;  TITLE OF INVENTION:  ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE:  CL000687
;  CURRENT APPLICATION NUMBER: US/60/212,664
;  CURRENT FILING DATE:  2000-06-20
;  NUMBER OF SEQ ID NOS:  636
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 118773
;   TYPE: DNA
;   ORGANISM: HUMAN
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(118773)
;   OTHER INFORMATION: n = A,T,C or G
US-60-212-664-10


  Query Match            90.0%;  Score 18;  DB 53;  Length 118773;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||
Db  60216 CCTGCTGCTCTTTCTGCT 60199


RESULT  12
US-60-212-664-251/c
; Sequence 251, Application US/60212664
; GENERAL INFORMATION:
;  APPLICANT:  Ladunga, Steve
;  APPLICANT:  Spier, Gene
;  APPLICANT:  Greenberg, Simon
;  APPLICANT:  Rabkin, Steven
;  APPLICANT:  Wang, Yu
;  TITLE OF INVENTION:  ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE:  CL000687
;  CURRENT APPLICATION NUMBER: US/60/212,664
;  CURRENT FILING DATE:  2000-06-20
;  NUMBER OF SEQ ID NOS:  636
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 251
;   LENGTH: 118773
;   TYPE: DNA
;   ORGANISM: HUMAN
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(118773)
;   OTHER INFORMATION: n = A,T,C or G
US-60-212-664-251


  Query Match            90.0%;  Score 18;  DB 53;  Length 118773;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||
Db  60216 CCTGCTGCTCTTTCTGCT 60199


RESULT  13
US-60-212-664-302/c
; Sequence 302, Application US/60212664
; GENERAL INFORMATION:
;  APPLICANT:  Ladunga, Steve
;  APPLICANT:  Spier, Gene
;  APPLICANT:  Greenberg, Simon
;  APPLICANT:  Rabkin, Steven
```

```
;  APPLICANT:  Wang, Yu
;  TITLE OF INVENTION:  ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE:  CL000687
;  CURRENT APPLICATION NUMBER: US/60/212,664
;  CURRENT FILING DATE:  2000-06-20
;  NUMBER OF SEQ ID NOS:  636
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 302
;   LENGTH: 118773
;   TYPE: DNA
;   ORGANISM: HUMAN
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(118773)
;   OTHER INFORMATION: n = A,T,C or G
US-60-212-664-302


  Query Match             90.0%;  Score 18;  DB 53;  Length 118773;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 CCTGCTGCTCTTTCTGCT 20
           ||||||||||||||||||
Db   60216 CCTGCTGCTCTTTCTGCT 60199


RESULT  14
US-60-217-080-9433/c
; Sequence 9433, Application US/60217080
; GENERAL INFORMATION:
;  APPLICANT:  Glenn, Matthew
;  APPLICANT:  Grigor, Murray R.
;  TITLE OF INVENTION:  Compositions isolated from bovine tissue
;  TITLE OF INVENTION:  and methods for their use.
;  FILE REFERENCE:  1051P2
;  CURRENT APPLICATION NUMBER: US/60/217,080
;  CURRENT FILING DATE:  2000-07-10
;  NUMBER OF SEQ ID NOS:  35169
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 9433
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Bovine
US-60-217-080-9433


  Query Match             87.0%;  Score 17.4;  DB 53;  Length 50;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCCTGCTGCTCTTTCTGCT 20
           |||||||||||  |||||||
Db      23 CCCTGCTGCTCCTTCTGCT 5


RESULT  15
US-09-540-733-6246
; Sequence 6246, Application US/09540733
; GENERAL INFORMATION:
;  APPLICANT:  Seilhamer, Jeffrey J.
;  APPLICANT:  Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.
;  APPLICANT:  Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.
;  APPLICANT:  Naughton, Rebecca E.
;  TITLE OF INVENTION:  POLYNUCLEOTIDES OF SKIN TISSUE
;  FILE REFERENCE:  PD-1035 CIP
;  CURRENT APPLICATION NUMBER: US/09/540,733
;  CURRENT FILING DATE:  2000-03-31
;  PRIOR APPLICATION NUMBER:  08/731,034
;  PRIOR FILING DATE:  October 2, 1996
;  PRIOR APPLICATION NUMBER:  60/004,674
;  PRIOR FILING DATE:  October 2, 1995
;  PRIOR APPLICATION NUMBER:  08/962,919
;  PRIOR FILING DATE:  October 23, 1997
;  PRIOR APPLICATION NUMBER:  60/029,306
;  PRIOR FILING DATE:  October 25, 1996
;  PRIOR APPLICATION NUMBER:  60/036,403
;  PRIOR FILING DATE:  January 21, 1997
;  PRIOR APPLICATION NUMBER:  08/806,593
;  PRIOR FILING DATE:  February 26, 1997
;  PRIOR APPLICATION NUMBER:  60/012,243
;  PRIOR FILING DATE:  February 26, 1996
;  PRIOR APPLICATION NUMBER:  08/941,884
;  PRIOR FILING DATE:  September 30, 1997
;  PRIOR APPLICATION NUMBER:  60/026,759
;  PRIOR FILING DATE:  October 3, 1996
;  NUMBER OF SEQ ID NOS:  7282
;  SOFTWARE:  PERL Program
; SEQ ID NO 6246
;   LENGTH: 305
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: hu01126643
US-09-540-733-6246


  Query Match             87.0%;  Score 17.4;  DB 21;  Length 305;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCCTGCTGCTCTTTCTGCT 20
           | ||||||||||||||||||
Db     197 cactgctgctctttctgct 215


Search completed: April 20, 2001, 03:21:32
Job time: 14179 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:15:48 ; Search time 101.94 Seconds
(without alignments)
27.149 Million cell updates/sec

Title: US-09-016-464-19
Perfect score: 20
Sequence: 1 GCCCTGCTGCTCTTTCTGCT 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 46985 seqs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	5	US-09-543-679A-1055	Sequence 1055, Ap
	2	20	100.0	156	5	US-09-543-679A-1735	Sequence 1735, Ap
c	3	20	100.0	1452	5	US-09-543-679A-2862	Sequence 2862, Ap
c	4	20	100.0	1489	5	US-09-543-679A-2865	Sequence 2865, Ap
c	5	20	100.0	2885	5	US-09-543-679A-2863	Sequence 2863, Ap
c	6	20	100.0	2918	5	US-09-543-679A-2867	Sequence 2867, Ap
	7	20	100.0	7033	5	US-09-543-679A-2411	Sequence 2411, Ap
	8	20	100.0	209274	5	US-09-543-679A-3004	Sequence 3004, Ap
c	9	17.4	87.0	782	5	US-09-739-449-1514	Sequence 1514, Ap
c	10	17.4	87.0	123654	6	US-60-248-505-41	Sequence 41, Appl
	11	16	80.0	8124	5	US-09-543-679A-2467	Sequence 2467, Ap
	12	16	80.0	9372	5	US-09-543-679A-3015	Sequence 3015, Ap
	13	16	80.0	35459	5	US-09-543-679A-3003	Sequence 3003, Ap
c	14	15.8	79.0	40090	5	US-09-820-004-3	Sequence 3, Appli
	15	15.8	79.0	58565	6	US-60-248-505-518	Sequence 518, App
	16	15.8	79.0	60415	6	US-60-248-505-194	Sequence 194, App
	17	15.8	79.0	68264	6	US-60-248-505-506	Sequence 506, App
	18	15.8	79.0	69428	6	US-60-248-505-576	Sequence 576, App
c	19	15.8	79.0	140825	6	US-60-248-505-571	Sequence 571, App
c	20	15.8	79.0	163502	6	US-60-248-505-221	Sequence 221, App
c	21	15.8	79.0	449171	6	US-60-248-505-42	Sequence 42, Appl
	22	15.8	79.0	479874	6	US-60-248-505-72	Sequence 72, Appl
	23	15.4	77.0	756	5	US-09-739-449-4605	Sequence 4605, Ap
	24	15.4	77.0	4474	6	US-60-248-505-1477	Sequence 1477, Ap
c	25	15.4	77.0	4651	6	US-60-248-505-1787	Sequence 1787, Ap
c	26	15.4	77.0	63957	5	US-09-739-449-196	Sequence 196, App
	27	15.4	77.0	90133	6	US-60-248-505-145	Sequence 145, App
	28	15.4	77.0	92126	6	US-60-248-505-455	Sequence 455, App
	29	15.4	77.0	101880	6	US-60-248-505-650	Sequence 650, App
c	30	15.4	77.0	142631	6	US-60-248-505-477	Sequence 477, App
c	31	15.4	77.0	183820	5	US-09-739-449-209	Sequence 209, App
c	32	15.4	77.0	259200	6	US-60-248-505-199	Sequence 199, App
c	33	15.2	76.0	236	4	US-08-276-163D-10433	Sequence 10433, A
	34	15.2	76.0	270	4	US-08-276-163D-15031	Sequence 15031, A
	35	15.2	76.0	502	4	US-08-276-163D-1181	Sequence 1181, Ap
c	36	15.2	76.0	1113	5	US-09-739-449-1530	Sequence 1530, Ap
c	37	15.2	76.0	1758	6	US-60-248-505-1408	Sequence 1408, Ap
	38	15.2	76.0	2022	5	US-09-813-206-882	Sequence 882, App
	39	15.2	76.0	5692	6	US-60-248-505-1982	Sequence 1982, Ap
	40	15.2	76.0	29445	6	US-60-248-505-76	Sequence 76, Appl
	41	15.2	76.0	32071	6	US-60-248-505-399	Sequence 399, App
c	42	15.2	76.0	101880	6	US-60-248-505-650	Sequence 650, App
c	43	15	75.0	257	4	US-08-276-163D-13103	Sequence 13103, A
c	44	14.8	74.0	377	5	US-09-487-566A-2214	Sequence 2214, Ap
	45	14.8	74.0	462	5	US-09-815-343-62	Sequence 62, Appl

ALIGNMENTS

```
RESULT   1
US-09-543-679A-1055
; Sequence 1055, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1055:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1055:
US-09-543-679A-1055


  Query Match             100.0%;  Score 20;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 GCCCTGCTGCTCTTTCTGCT 20


RESULT   2
US-09-543-679A-1735
; Sequence 1735, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1735:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 156 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1735:
US-09-543-679A-1735


  Query Match             100.0%;  Score 20;  DB 5;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db      1 GCCCTGCTGCTCTTTCTGCT 20


RESULT   3
US-09-543-679A-2862/c
; Sequence 2862, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2862:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1452 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2862:
US-09-543-679A-2862


  Query Match             100.0%;  Score 20;  DB 5;  Length 1452;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db    110 GCCCTGCTGCTCTTTCTGCT 91


RESULT   4
US-09-543-679A-2865/c
; Sequence 2865, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
```

```
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2865:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1489 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2865:
US-09-543-679A-2865


  Query Match            100.0%;  Score 20;  DB 5;  Length 1489;
  Best Local Similarity  100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db    110 GCCCTGCTGCTCTTTCTGCT 91


RESULT   5
US-09-543-679A-2863/c
; Sequence 2863, Application US/09543679A
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2863:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2885 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2863:
US-09-543-679A-2863


  Query Match            100.0%;  Score 20;  DB 5;  Length 2885;
  Best Local Similarity  100.0%;  Pred. No. 1.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db   1543 GCCCTGCTGCTCTTTCTGCT 1524


RESULT   6
US-09-543-679A-2867/c
; Sequence 2867, Application US/09543679A
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2867:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2918 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2867:
US-09-543-679A-2867


  Query Match            100.0%;  Score 20;  DB 5;  Length 2918;
  Best Local Similarity  100.0%;  Pred. No. 1.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGCT 20
          ||||||||||||||||||||
Db    804 GCCCTGCTGCTCTTTCTGCT 785


RESULT   7
US-09-543-679A-2411
; Sequence 2411, Application US/09543679A
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
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;                          COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                          OF AIRWAY DISORDERS ASSOCIATED WITH
;                          BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2411:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 7033 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2411:
US-09-543-679A-2411


  Query Match             100.0%;  Score 20;  DB 5;  Length 7033;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCCCTGCTGCTCTTTCTGCT 20
           ||||||||||||||||||||
Db      82 GCCCTGCTGCTCTTTCTGCT 101


RESULT   8
US-09-543-679A-3004
; Sequence 3004, Application US/09543679A
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                          COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                          OF AIRWAY DISORDERS ASSOCIATED WITH
;                          BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3004:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 209274 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3004:
US-09-543-679A-3004


  Query Match             100.0%;  Score 20;  DB 5;  Length 209274;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCCCTGCTGCTCTTTCTGCT 20
           ||||||||||||||||||||
Db      82 GCCCTGCTGCTCTTTCTGCT 101


RESULT   9
US-09-739-449-1514/c
; Sequence 1514, Application US/09739449
; GENERAL INFORMATION:
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15490)C
;  CURRENT APPLICATION NUMBER: US/09/739,449
;  CURRENT FILING DATE:  2000-12-19
;  PRIOR APPLICATION NUMBER: US 09/514,000
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 1514
;   LENGTH: 782
;   TYPE: DNA
;   ORGANISM: Agrobacterium tumefaciens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(782)
;   OTHER INFORMATION: unsure at all n locations
US-09-739-449-1514


  Query Match             87.0%;  Score 17.4;  DB 5;  Length 782;
  Best Local Similarity   94.7%;  Pred. No. 19;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCCTGCTGCTCTTTCTGCT 20
           |||||||||||||  |||||
Db     449 CCCTGCTGCTCTTCCTGCT 431


RESULT  10
US-60-248-505-41/c
; Sequence 41, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
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;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: cl000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 123654
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(123654)
;   OTHER INFORMATION: n = A,T,C or G
US-60-248-505-41


  Query Match             87.0%;  Score 17.4;  DB 6;  Length 123654;
  Best Local Similarity   94.7%;  Pred. No. 28;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
          |||||||||||| |||||
Db  49152 CCCTGCTGCTCTTCCTGCT 49134


RESULT  11
US-09-543-679A-2467
; Sequence 2467, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2467:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 8124 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2467:
US-09-543-679A-2467


  Query Match             80.0%;  Score 16;  DB 5;  Length 8124;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCT 17
          ||||||||||||||||
Db   5177 CCCTGCTGCTCTTTCT 5192


RESULT  12
US-09-543-679A-3015
; Sequence 3015, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3015:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9372 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3015:
US-09-543-679A-3015


  Query Match             80.0%;  Score 16;  DB 5;  Length 9372;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCT 17
          ||||||||||||||||
Db   5744 CCCTGCTGCTCTTTCT 5759


RESULT  13
US-09-543-679A-3003
; Sequence 3003, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
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```
;                          BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3003:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 35459 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3003:
US-09-543-679A-3003


  Query Match             80.0%;  Score 16;  DB 5;  Length 35459;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCT 17
          ||||||||||||||||
Db  15877 CCCTGCTGCTCTTTCT 15892


RESULT  14
US-09-820-004-3/c
; Sequence 3, Application US/09820004
; GENERAL INFORMATION:
;  APPLICANT: WEI, Ming-Hui et al.
;  TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001201
;  CURRENT APPLICATION NUMBER: US/09/820,004
;  CURRENT FILING DATE:  2001-03-29
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 40090
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(40090)
;   OTHER INFORMATION: n = A,T,C or G
US-09-820-004-3


  Query Match             79.0%;  Score 15.8;  DB 5;  Length 40090;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 CCCTGCTGCTCTTTCTGCT 20
          |||||||||||||| | ||
Db   5696 CCCTGCTGCTCTTTTTCCT 5678


RESULT  15
US-60-248-505-518
; Sequence 518, Application US/60248505
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: c1000918
;  CURRENT APPLICATION NUMBER: US/60/248,505
;  CURRENT FILING DATE:  2000-11-15
;  NUMBER OF SEQ ID NOS: 1998
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 518
;   LENGTH: 58565
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(58565)
;   OTHER INFORMATION: n = A,T,C or G
US-60-248-505-518


  Query Match             79.0%;  Score 15.8;  DB 6;  Length 58565;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GCCCTGCTGCTCTTTCTGC 19
          ||| |||||||||| ||||
Db  26422 gccttgctgctcttcctgc 26440



Search completed: April 20, 2001, 00:15:57
Job time: 9494 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:00:29 ; Search time 2028.86 Seconds
(without alignments)
57.668 Million cell updates/sec

Title: US-09-016-464-20
Perfect score: 19
Sequence: 1 GCGCTCGGCCTGGTCCCGG 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
16: em_ba1:*
17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
21: em_htgo_rod:*
22: em_htg_hum1:*
23: em_htg_hum2:*
24: em_htg_hum3:*
25: em_htg_hum4:*
26: em_htg_hum5:*
27: em_htg_hum6:*
28: em_htg_hum7:*
29: em_htg_hum8:*
30: em_htg_inv1:*
31: em_htg_inv2:*
32: em_htg_other:*
33: em_htg_rod:*
34: em_hum1:*
35: em_hum2:*
36: em_hum3:*
37: em_hum4:*
38: em_hum5:*
39: em_hum6:*
40: em_hum7:*
41: em_in:*
42: em_om:*
43: em_or:*
44: em_ov:*
45: em_pat:*
46: em_ph:*
47: em_pl:*
48: em_ro:*
49: em_sts:*
50: em_sy:*
51: em_un:*
52: em_vi:*
53: gb_sts1:*
54: gb_sts2:*
55: gb_sts3:*
56: gb_sy:*
57: gb_un:*
58: gb_vi1:*
59: gb_vi2:*
60: gb_htg1:*
61: gb_htg2:*
62: gb_htg3:*
63: gb_htg4:*
64: gb_htg5:*
65: gb_htg6:*
66: gb_htg7:*
67: gb_htg8:*
68: gb_htg9:*
69: gb_htg10:*
70: gb_htg11:*
71: gb_htg12:*
72: gb_htg13:*
73: gb_htg14:*
74: gb_htg15:*
75: gb_htg16:*
76: gb_htg17:*
77: gb_htg18:*
78: gb_htg19:*
79: gb_htg20:*
80: gb_htg21:*
81: gb_htg22:*
82: gb_htg23:*
83: gb_htg24:*
84: gb_htg25:*
85: gb_pr1:*
86: gb_pr2:*
87: gb_pr3:*
88: gb_pr4:*
89: gb_pr5:*
90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_ro1:*
95: gb_ro2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	19	100.0	429	93	HUMEPP03	M29906 Homo sapien
c 2	19	100.0	2558	92	HSEP	X14346 Human mRNA
c 3	19	100.0	162083	86	AC005962	AC005962 Homo sapi
c 4	17.4	91.6	4265	1	AB028210	AB028210 Streptomy
5	17.4	91.6	17856	3	SCK20	AL450450 Streptomy
c 6	17.4	91.6	32274	3	SCC8A	AL356892 Streptomy
c 7	17.4	91.6	191877	86	AC007207	AC007207 Homo sapi
8	17.4	91.6	201290	77	AC084375	AC084375 Homo sapi
c 9	17.4	91.6	300691	60	AC005842	AC005842 Homo sapi
c 10	16.4	86.3	2963	11	BPD3112AB	X87627 Bacteriopha
c 11	16.4	86.3	3611	1	AF099190	AF099190 Caulobact

c	12	16.4	86.3	4988	3	U18133	U18133 Comamonas t
	13	16.4	86.3	6927	2	AF319543	AF319543 Streptomy
	14	16.4	86.3	8300	3	SCARGGH	Z49111 Streptomyce
	15	16.4	86.3	36583	3	SC5H1	AL049863 Streptomy
c	16	16.4	86.3	40476	3	SCC75A	AL133220 Streptomy
	17	16.4	86.3	44109	3	SC5F1	AL450165 Streptomy
c	18	16.4	86.3	139544	92	HSDJ85M6	AL121926 Human DNA
c	19	16.4	86.3	147664	78	AL138691	AL138691 Homo sapi
	20	16.4	86.3	176306	71	AC032013	AC032013 Mus muscu
c	21	16.4	86.3	178353	63	AC012334	AC012334 Homo sapi
c	22	16.4	86.3	183663	80	AL356961	AL356961 Homo sapi
	23	16	84.2	17124	1	AE004789	AE004789 Pseudomon
c	24	16	84.2	68000	78	AC090053	AC090053 Leishmani
	25	16	84.2	110000	84	LMFLCHR32_09	Continuation (10 o
	26	16	84.2	349116	2	AP003003	AP003003 Mesorhizo
	27	15.8	83.2	400	54	G16330	G16330 human STS S
	28	15.8	83.2	593	2	AF228524	AF228524 Streptomy
	29	15.8	83.2	632	12	AF058476	AF058476 Eucalyptu
c	30	15.8	83.2	719	53	CNS01NQG	AL152553 Anopheles
c	31	15.8	83.2	996	53	CNS01LFY	AL149583 Anopheles
c	32	15.8	83.2	1046	53	CNS01LCF	AL149456 Anopheles
c	33	15.8	83.2	1200	94	RATCELF	M65149 Rat CELF mR
	34	15.8	83.2	1284	3	PAAZUR	X07317 Pseudomonas
	35	15.8	83.2	1287	3	PSEAZU	M30389 Pseudomonas
	36	15.8	83.2	1401	9	AR058223	AR058223 Sequence
	37	15.8	83.2	1401	93	HUMNUCTIAR	M96954 Homo sapien
	38	15.8	83.2	1826	88	AF113527	AF113527 Homo sapi
c	39	15.8	83.2	1837	1	AF010151	AF010151 Pseudomon
c	40	15.8	83.2	2059	7	AF319658	AF319658 Sus scrof
	41	15.8	83.2	2417	3	PDNORNOZ	X74792 P.denitrifi
	42	15.8	83.2	2628	1	AF193856	AF193856 Streptomy
	43	15.8	83.2	2750	15	ZMU82481	U82481 Zea mays KI
	44	15.8	83.2	2988	8	GDJUNDG	X60063 G.domesticu
c	45	15.8	83.2	3395	94	MMECK	X78339 M.musculus

ALIGNMENTS

```
RESULT   1
HUMEPP03/c
LOCUS       HUMEPP03      429 bp    DNA             PRI       23-OCT-2000
DEFINITION  Homo sapiens eosinophil peroxidase (EPP) gene, exons 4 and 5.
ACCESSION   M29906 M86682
VERSION     M29906.1  GI:182137
KEYWORDS    eosinophil peroxidase.
SEGMENT     3 of 10
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 429)
  AUTHORS   Sakamaki,K., Tomonaga,M., Tsukui,K. and Nagata,S.
  TITLE     Molecular cloning and characterization of a chromosomal gene for
            human eosinophil peroxidase
  JOURNAL   J. Biol. Chem. 264 (28), 16828-16836 (1989)
  MEDLINE   89380315
FEATURES             Location/Qualifiers
     source          1. .429
                     /organism="Homo sapiens"
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     intron          <1. .13
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     intron          132. .262
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     exon            263. .392
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ORIGIN


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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
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Db      87 GCGCTCGGCCTGGTCCCGG 69


RESULT   2
HSEP/c
LOCUS       HSEP          2558 bp    mRNA            PRI       14-JUL-1995
DEFINITION  Human mRNA for eosinophil peroxidase.
ACCESSION   X14346
VERSION     X14346.1  GI:31182
KEYWORDS    eosinophil peroxidase; peroxidase.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2558)
  AUTHORS   Rosa,M.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-FEB-1989) Rosa M.T., Mayo Clinic and Foundation, 406
            Guggenheim Building, Rochester, MN 55905
REFERENCE   2  (bases 1 to 2558)
  AUTHORS   Ten,R.M., Pease,L.R., McKean,D.J., Bell,M.P. and Gleich,G.J.
  TITLE     Molecular cloning of the human eosinophil peroxidase. Evidence for
            the existence of a peroxidase multigene family
  JOURNAL   J. Exp. Med. 169 (5), 1757-1769 (1989)
  MEDLINE   89235593
COMMENT     Data kindly reviewed (23-aug-1989) by Gleich G.J.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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     CDS             <1. .2109
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                     GLSQPRNLAQLSRVLKNQDLARKFLNLYGTPDNIDIWIGAIAEPLLPGARVGPLLACL
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     mat_peptide     382. .2106
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     misc_feature    715. .2106
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BASE COUNT      527 a    820 c    698 g    513 t
ORIGIN


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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
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Db    384 GCGCTCGGCCTGGTCCCGG 366


RESULT   3
AC005962/c
LOCUS       AC005962   162083 bp    DNA             PRI       24-NOV-1998
DEFINITION  Homo sapiens chromosome 17, clone hRPK.506_H_21, complete sequence.
ACCESSION   AC005962
VERSION     AC005962.1  GI:3924656
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 162083)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone hRPK.506_H_21
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 162083)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boutwell,C.,
            Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins,S.,
            Collymore,A., Cooke,P., Corliss,D., Depayre,E., Devon,K., Dewar,K.,
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            Severy,P., Stange-Thomann,N., Stilwell,J., Stojanovic,N., Stone,C.,
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            Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,Y., Wyman,D.,
            Ye,W.J., Zhao,J. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-NOV-1998) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 162083)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boutwell,C.,
            Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins,S.,
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            Subramanian,A., Tesfaye,S., Tichovolsky,N., Torruella-Miller,I.,
            Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,Y., Wyman,D.,
            Ye,W.J., Zhao,J. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-NOV-1998) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Nov 24, 1998 this sequence version replaced gi:3907449.
            All repeats were identified using RepeatMasker: Smit, A.F.A. &
            Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html

            Only the first 162083 base pairs of this clone are being submitted.
            The remainder overlaps accession number AC004687 (WICGR project
            L319).
FEATURES             Location/Qualifiers
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Qy       1 GCGCTCGGCCTGGTCCCGG 19
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Db  115409 GCGCTCGGCCTGGTCCCGG 115391


RESULT   4
AB028210/c
LOCUS       AB028210     4265 bp    DNA             BCT       10-JUN-1999
DEFINITION  Streptomyces griseus hya and kan genes for hyaluronidase and
            aminoglycoside 3-N-acetyltransferase, complete cds.
ACCESSION   AB028210 D00681
VERSION     AB028210.1  GI:5002503
KEYWORDS    aminoglycoside 3-N-acetyltransferase; hyaluronidase.
SOURCE      Streptomyces griseus DNA.
  ORGANISM  Streptomyces griseus
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE   1  (bases 1 to 4265)
  AUTHORS   Ishikawa,J. and Hotta,K.
  TITLE     Identification of a hyaluronidase gene in Streptomyces griseus
            SS-1198PR
  JOURNAL   Published Only in DataBase (1999) In press
REFERENCE   2  (bases 1 to 4265)
  AUTHORS   Ishikawa,J. and Hotta,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUN-1999) to the DDBJ/EMBL/GenBank databases. Jun
            Ishikawa, National Institute of Infectious Diseases, Department of
            Bioactive Molecules; 1-23-1 Toyama, Shinjuku, Tokyo 162-8640, Japan
            (E-mail:jun@nih.go.jp, URL:http://www.nih.go.jp/niid/index-e.html,
            Tel:81-3-5285-1111(ex.2354), Fax:81-3-5285-1272)
FEATURES             Location/Qualifiers
     source          1. .4265
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     CDS             523. .2688
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                     MYDAIAQERLARYCAAVDHFVPDSAVASYTGTSTGANRVDLCRVLALRGVVGGRRRRS
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                     RLFPDMARATHRRPGWAASLSMADRRVTYYEAGNGENLRGWHTGSGMLYWWGDTFANG
                     QYSDAFWPTVDPYRLPGTTASRKVLADGAGGDWGVSLPDVNWVGGVTDSKRAAVGQYL
                     KGLTSTLMAKKSWFFLDDTVVCLGAGIHGRDGAAVETTVDNRNLGPTGNAPFTVDGSV
                     KPLTLPWSATLTGASWAHLAGHGGYVFPGGATVKALREDRTGRWRDINKAGSTDPVSR
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                     RLTAVNFWFGGTVGPLVADAPCSVMVTEHADGTATVCVSDPMRARTSLTLTWNRAVAS
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ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 4265;
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Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 3493 GCGCTCGGCCTCGTCCCGG 3475

RESULT 5
SCK20
LOCUS SCK20 17856 bp DNA BCT 01-DEC-2000
DEFINITION Streptomyces coelicolor cosmid K20.
ACCESSION AL450450
VERSION AL450450.1 GI:11544744
KEYWORDS ECF sigma factor; integral membrane protein; lipoprotein; membrane protein; monooxygenase; mutA2, methylmalonyl CoA mutase; secreted hydrolase; tetR-family transcriptional regulator; transferase.
SOURCE Streptomyces coelicolor.
ORGANISM Streptomyces coelicolor
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE 1 (bases 1 to 17856)
AUTHORS Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J., Kinashi,H. and Hopwood,D.A.
TITLE A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
JOURNAL Mol. Microbiol. 21 (1), 77-96 (1996)
MEDLINE 97000351
REFERENCE 2 (bases 1 to 17856)
AUTHORS Seeger,K. and Harris,D.
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 17856)
AUTHORS Cerdeno,A.M., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
COMMENT Notes:
Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary strand).
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid K20 overlaps with cosmid St5G8 and cosmid 2StK8.
FEATURES Location/Qualifiers
source 1. .17856
/organism="Streptomyces coelicolor"
/db_xref="taxon:1902"
gene 1. .1398
/gene="SCK20.01"
source 1. .17856
/organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
/db_xref="taxon:100226"
/clone="cosmid K20"
CDS <1. .1398
/gene="SCK20.01"
/note="SCK20.01, probable secreted hydrolase (fragment), len: >465 aa; similar to C-terminal region of SW:HEXA_DICDI (EMBL:J04065) Dictyostelium discoideum beta-hexosaminidase A precursor (EC 3.2.1.52) NagA, 532 aa; fasta scores: opt: 343 z-score: 387.7 E(): 4.6e-14; 25.4% identity in 393 aa overlap. Contains Pfam match to entry PF00728 Glyco_hydro_20, Glycosyl hydrolase family 20"
/codon_start=1
/transl_table=11
/product="putative secreted hydrolase (fragment)"
/protein_id="CAC17648.1"
/db_xref="GI:11544745"
/translation="PAVREHTAARGPGWQPEKGNRVVVADSGLADEGKQIAGDLGMTY
AGEKDDERAGDLLLDVKAAKGANPESYTMTVRDGRVTVTGPAEAGVYYGTRTLKQAVD
GGGTAPEGVVKDEPAKPKRGFSLDIARKHYSADWIKDRIRELGDLKFNELGLHFSDDQ
AFRIESDSHPEIVSDEHLTKAEMKEIIDLAASRHITVVPEIDSPGHLGAVIAAHPDLQ
LRNAQGTATRGAIDISKPEAAKIVDDLLNEYADLFPGSQFHLGADEYQALVVPNPEAS
YPTLAAAARKAYGSGGTVADLTTGWLNGRAKTVMAHDRTPRAWNDGFFKDTSVEPLKD
IKVAYWTGKEIGARPPAEYLGEGRQVLNYNDEFLYYVLGQPQTFVYPTGERIYEQWTP
RVLRGTTAVDAKYDDQILGGSFAVWGDFPNAQTQAQVAEGIRLPLAATVQKLWDPGKP
ELSWTDFAALANRLD"
misc_feature 1. .108
/gene="SCK20.01"
/note="nominal overlap with Streptomyces coelicolor cosmid SC5G8"
misc_feature 205. .792
/gene="SCK20.01"
/note="Pfam match to entry PF00728 Glyco_hydro_20, Glycosyl hydrolase family 20, score 71.80, E-value 1.9e-18"
gene 1517. .2062
/gene="SCK20.02"
CDS 1517. .2062
/gene="SCK20.02"
/note="SCK20.02, unknown, len: 181 aa"
/codon_start=1
/transl_table=11
/product="hypothetical protein SCK20.02"
/protein_id="CAC17649.1"
/db_xref="GI:11544746"
/translation="MGYWGYFVVGRAERPLAELEALSGAGDMTLRQSAPDGWQVWEFP
GGDGDVGNMNDLAGQTGAPALFGYVMDSDCVVVEAAAPESGAWTTCLARTAMAGYLGA
ERDGLTLEDYFLEPRDAAERAVAWAAEAGCAASPAELAGVLSDDPAAEPDAGGDRVLA
PGPVAENLFFRFLDRLGVVPL"
RBS 2139. .2143
gene 2150. .2719
/gene="SCK20.03"
CDS 2150. .2719
/gene="SCK20.03"
/note="SCK20.03, unknown, len: 189 aa"
/codon_start=1
/transl_table=11

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                /product="hypothetical protein SCK20.03"
                /protein_id="CAC17650.1"
                /db_xref="GI:11544747"
                /translation="MSLVELIARADTRGLAASGLACLDRCVPLLDGDDEALRPLWATL
                ADASGDASGPDWAEALAQVRDKLAGPGATGEDEAAVLARRMLAAAPAECSGPVLRTWA
                DACSVASLRIHRLLAPAAGAAPEADVPRDAGTEGLPPLVAAELRRQAAVLELLAGHGA
                AGVRPALEVSTEGRRVLRAVVSRRARGRG"
gene            2887. .3309
                /gene="SCK20.04"
CDS             2887. .3309
                /gene="SCK20.04"
                /note="SCK20.04, unknown, len: 140 aa"
                /codon_start=1
                /transl_table=11
                /product="hypothetical protein SCK20.04"
                /protein_id="CAC17651.1"
                /db_xref="GI:11544748"
                /translation="MTSGLTSGWTSGTTSPQQPRPSAAARPVRWAADAVATMREGARL
                RLDYSAQSLWRVDRMIDGIRGEEAPYAAVETALRGLGAYAGEVIVRQSGGEWWTTGGD
                HWVRTPDGRLWDPIDEARRCFAGDGSLRLLCRDATAPR"
gene            3376. .4053
                /gene="SCK20.05"
CDS             3376. .4053
                /gene="SCK20.05"
                /note="SCK20.05, possible ECF sigma factor, len: 225 aa;
                similar to TR:Q9RIT1 (EMBL:AJ010584) Streptomyces
                coelicolor ECF sigma factor, 264 aa; fasta scores: opt:
                296 z-score: 342.7 E(): 1.5e-11; 34.0% identity in 212 aa
                overlap and to Streptomyces coelicolor putative ECF sigma
                factor SCK20.07, 220 aa; fasta scores: opt: 671 z-score:
                656.4 E(): 6.9e-31; 59.5% identity in 185 aa overlap.
                Contains Pfam match to entry PF00776 Sigma70_ECF, Sigma-70
                factor (ECF subfamily)"
                /codon_start=1
                /transl_table=11
                /product="putative ECF sigma factor"
                /protein_id="CAC17652.1"
                /db_xref="GI:11544749"
                /translation="MTLGGAHRSARRTRYGRGRFLGQRGEPRRVQAYDGELGAAVARA
                QQGDEAAFAVAYRLVQPGLLGYVRGLVGEDAEDVAADAWLEIARDLRRFKGDGAGFRG
                WTATIARHRALDHLRRQKVRPRPTALEQDVLDLPGPHSTHEQVLETLSTRAALGLVAA
                LPRDQAEAVLLRVVVGLDGPSAARVLGKRPGAVRTATYRGLKRLARQLGADGVTDDGP
                RTLGEST"
misc_feature    3568. .3732
                /gene="SCK20.05"
                /note="Pfam match to entry PF00776 Sigma70_ECF, Sigma-70
                factor (ECF subfamily), score 34.80, E-value 1.9e-06"
RBS             4041. .4044
                /gene="SCK20.05"
gene            4050. .4970
                /gene="SCK20.06"
CDS             4050. .4970
                /gene="SCK20.06"
                /note="SCK20.06, unknown, len: 306 aa. High G+C content
                (82.13%)"
                /codon_start=1
                /transl_table=11
                /product="hypothetical protein SCK20.06"
                /protein_id="CAC17653.1"
                /db_xref="GI:11544750"
                /translation="MRGAAGGGPADRAGAEADMGARHEAGDGRDTGPRPAPGGVPGTE
                ALLAAALRAESAGTEGERRALAAFRAARDAEPARAARTRRRDDWRPRDGRHQGRTPRT
                ALSVLLASLTLGGVAYAAMGGGGSASDDGGPDRTRPPAVSDDAPARPAATPPGTTPGP
                GTTGPATTPPGASESPGTSAPPRVSTPPGPPSVGRDTEAQCRVYERLAGNGKSLDAAA
                WRRLVAAAGGAERVETYCADQLDRLGLPTGPGPSTGAGNGTGGNDAGNGGTGDTGTEG
                GAGGILGDGGADPEAGDGGIAAQVPDLDHP"
misc_feature    4446. .4622
                /gene="SCK20.06"
                /note="High content in proline, threonine and alanine
                amino acid residues. High content in G+C (86.44%)"
gene            5354. .6016
                /gene="SCK20.07"
CDS             5354. .6016
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  Query Match             91.6%;  Score 17.4;  DB 3;  Length 17856;
  Best Local Similarity   94.7%;  Pred. No. 5.5e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           ||||||||||||||| |||
Db    3835 GCGCTCGGCCTGGTCGCGG 3853
```

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RESULT   6
SCC8A/c
LOCUS       SCC8A       32274 bp    DNA             BCT       26-MAY-2000
DEFINITION  Streptomyces coelicolor cosmid G8.
ACCESSION   AL356892
VERSION     AL356892.1  GI:8246783
KEYWORDS    acetyltransferase; ATP/GTP-binding; DedA-family; hydrolase;
            integral membrane transport; lipoprotein; peptidodoglycan-binding;
            pyruvate dehydrogenase E1 component; sensor kinase; tcmA;
            tetracenomycin C efflux protein; thiol-specific antioxidant; tRNA;
            two-component response regulator.
SOURCE      Streptomyces coelicolor A3(2).
  ORGANISM  Streptomyces coelicolor A3(2)
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE   1  (bases 1 to 32274)
  AUTHORS   Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
            Kinashi,H. and Hopwood,D.A.
  TITLE     A set of ordered cosmids and a detailed genetic and physical map
            for the 8 Mb Streptomyces coelicolor A3(2) chromosome
  JOURNAL   Mol. Microbiol. 21 (1), 77-96 (1996)
  MEDLINE   97000351
REFERENCE   2  (bases 1 to 32274)
  AUTHORS   Brown,S.P. and Harris,D.
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 32274)
  AUTHORS   Bentley,S.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAY-2000) Streptomyces coelicolor sequencing project,
            Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
            CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
            David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
            Colney, Norwich, Norfolk NR4 7UH, UK
COMMENT     Notes:
            Streptomyces coelicolor sequencing at The Sanger Centre is funded
            by the BBSRC and Beowulf Genomics
            Details of S. coelicolor sequencing at the Sanger Centre are
            available on the World Wide Web.
            (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
            CDS are numbered using the following system eg SC7B7.01c. SC (S.
            coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
            strand).
            The more significant matches with motifs in the PROSITE database
            are also included but some of these may be fortuitous.
            The length in codons is given for each CDS.
            Usually the highest scoring match found by fasta -o is given for
            CDS which show significant similarity to other CDS in the database.
            The position of possible ribosome binding site sequences are given
            where these have been used to deduce the initiation codon.
            Gene prediction is based on positional base preference in codons
            using a specially developed Hidden Markov Model (Krogh et al.,
            Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot
            program of Bibb et al., Gene 30:157-66(1984) as implemented at
            http://www.nih.go.jp/
            jun/cgi-bin/frameplot.pl. CAUTION:  We may not have predicted the
            correct initiation codon.  Where possible we choose an initiation
            codon (atg, gtg, ttg or (att)) which is preceded by an upstream
            ribosome binding site sequence (optimally 5-13bp before the
            initiation codon).  If this cannot be identified we choose the most
            upstream initiation codon.
            IMPORTANT: This sequence MAY NOT be the entire insert of the
            sequenced clone.  It may be shorter because we only sequence
            overlapping sections once, or longer, because we arrange for a
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          small overlap between neighbouring submissions.
          Cosmid C8A.
FEATURES             Location/Qualifiers
     source          1. .32274
                     /organism="Streptomyces coelicolor A3(2)"
                     /strain="A3(2)"
                     /db_xref="taxon:100226"
                     /clone="cosmid C8A"
     misc_feature    1. .100
                     /note="Nominal overlap with Streptomyces coelicolor cosmid
                     C53"
     gene            184. .717
                     /gene="SCC8A.01"
     CDS             184. .717
                     /gene="SCC8A.01"
                     /note="SCC8A.01, possible acetyltransferase, len: 177aa;
                     similar to many of undefined function eg. TR:CAB59671
                     (EMBL:AL132674) putative acetyltransferase from
                     Streptomyces coelicolor (161 aa) fasta scores; opt: 194,
                     z-score: 245.6, E(): 3.2e-06, 33.3% identity in 165 aa
                     overlap. Contains Pfam match to entry PF00583
                     Acetyltransf, Acetyltransferase (GNAT) family, score
                     44.30, E-value 2.7e-09."
                     /codon_start=1
                     /transl_table=11
                     /product="putative acetyltransferase"
                     /protein_id="CAB92819.1"
                     /db_xref="GI:8246784"
                     /translation="MTWTVDPEPYDSPVAAALWRAYYTEVSDRWYRLHEGRATDPDEL
                     EREIAAYPGADLVPPRGRLLVARYGGEPAGSSGVRLLDHTTAELTRVFLYGPMRGRGG
                     AALLVRAAEDAARALGAERMVLDTRGDLVEARALYARLGYTETEAYNESPYAEHWFAK
                     RLRSDRDYRRPRSDRGS"
     misc_feature    193. .612
                     /gene="SCC8A.01"
                     /note="Pfam match to entry PF00583 Acetyltransf,
                     Acetyltransferase (GNAT) family, score 44.30, E-value
                     2.7e-09"
     repeat_region   674. .754
                     /note="3x CCGACCGCGacTcCtGACGgCcgCGCT repeat"
     gene            complement(754. .2823)
                     /gene="SCC8A.02c"
     CDS             complement(754. .2823)
                     /gene="SCC8A.02c"
                     /note="SCC8A.02c, possible integral membrane transport
                     protein, len: 689aa; similar to many eg. TR:CAB89031
                     (EMBL:AL353870) putative membrane transport protein from
                     Streptomyces coelicolor (714 aa) fasta scores; opt: 1767,
                     z-score: 1907.0, E(): 0, 46.1% identity in 670 aa overlap
                     and TR:P96712 (EMBL:D50098) multidrug transporter from
                     Bacillus subtilis (512 aa) fasta scores; opt: 1168,
                     z-score: 1262.8, E(): 0, 37.6% identity in 495 aa overlap.
                     Contains Pfam match to entry PF00083 sugar_tr, Sugar (and
                     other) transporter and possible membrane-spanning
                     hydrophobic regions."
                     /codon_start=1
                     /transl_table=11
                     /product="putative integral membrane transport protein"
                     /protein_id="CAB92820.1"
                     /db_xref="GI:8246785"
                     /translation="MAGDVREATESEPDPARPAAPGEREQVSSGVLVSIGALLLGMLL
                     AALDQTIVSTALPTIVSDLGGLEHLSWVVTAYLLAATAATPLWGKLGDQYGRKKLFQL
                     AIGIFLVGSALCGIAQGMGQLIAFRALQGLGGGGLMVLSMAIVGDLVPPRERGRYQGL
                     FGAVFGATSVLGPLLGGVFTEHLSWRWVFYINLPIGVVALAVIAAVLHIPRRTTRHVI
                     DYLGTLLIASVATSLVLVASLGGTTWAWSSPQIIGLAVLAVVLAVLFVAVERRAAEPV
                     LPLKLFRVRTFALSAVISFVIGFAMFGAMTYLPTFLQVVRGVTPTMSGVYMLPMVFGL
                     LLSSTVSGQIVSRTGRWKVFPVAGTAVTTLGLLLLHQLDENSATAEMGAYFFVFGLGL
                     GLVMQVLVLIVQNAVAYEDLGVATSGATFFRSIGASFGVAIFGTIFASRLGDQLTDAF
                     RGAALPPGVSVDTLKADPRGIGALPPALRPEAIHAYASSITDVFLYAAPVALLAFLLA
                     WLLKEDRLRGSVTAPDATQTLASNPVERSSHDEVCRALSVLGTREGRREIYRRITARA
                     GYDLLPASSWMLLRVRKYGRVEPAQLAERSPVPLATVMAAARQVEERHLAVREGPDLV
                     LTRQGREVAERLALAREESLAELLGDWWGPDRPTDLVRLVRELTGELCGSERERPHEG
                     RTPARAG"
     misc_feature    complement(1363. .2727)
                     /gene="SCC8A.02c"
                     /note="Pfam match to entry PF00083 sugar_tr, Sugar (and
                     other) transporter, score -80.20, E-value 0.00054"
     RBS             complement(2828. .2833)
     RBS             2859. .2862
     gene            2872. .4230
                     /gene="SCC8A.03"
     CDS             2872. .4230
                     /gene="SCC8A.03"
                     /note="SCC8A.03, possible peptidodoglycan-binding membrane
                     protein, len: 452aa; contains Pfam match to entry PF01471
                     PG_binding_1, Putative peptidoglycan binding domain, score
                     35.30, E-value 1.4e-06 and possible membrane-spanning
                     hydrophobic region."
                     /codon_start=1
                     /transl_table=11
                     /product="putative peptidodoglycan-binding membrane
                     protein"
                     /protein_id="CAB92821.1"
                     /db_xref="GI:8246786"
                     /translation="MAVSVLREAGIPGACAPKYGEDLHNLWRSRGGREGRDERVDQQK
                     EPSQDRPAGAACPECGTPRAADNTPSCACGTRASDALRDARTAQAAAAEDFDPLRIRP
                     YVELDGTAGDPSGAPDASDAAGASGEHLVPPASPTPPASPVPPASPGSDPDATMTLRA
                     VGAGAGAGAGAGAGAGAGTGAASGSDPRDGDMEAASALPTPLAPSAGSPSAHDLRL
                     FDASATTPLPRADPGRGGAGGDGGPPRRRRRGVLLSAAGAVVVVIGAAGFASGLFSYD
                     TPSRDGAMPDEVRASVPDPSTGESSPSAEPSASSASPSPSASASPSASASPSASDSAS
                     ASPSPSASASSASPTPSRSAEPSQSTTTPADDAPQESGDDDSPDGGTLSRGDQGPEVV
                     ELQQRLKEKWMYWGDLDGDYDRQVEDAVRQYQWENRIRTDRVGVYGPDTRRKLESETR
                     EP"
     misc_feature    4030. .4218
                     /gene="SCC8A.03"
                     /note="Pfam match to entry PF01471 PG_binding_1, Putative
                     peptidoglycan binding domain, score 35.30, E-value
                     1.4e-06"
     gene            complement(4269. .4934)
                     /gene="SCC8A.04c"
     CDS             complement(4269. .4934)
                     /gene="SCC8A.04c"
                     /note="SCC8A.04c, possible hydrolase, len: 221aa; similar
                     to many eg. TR:P96428 (EMBL:Z79692) ORF24 from
                     Sinorhizobium meliloti (233 aa) fasta scores; opt: 526,
                     z-score: 576.9, E(): 1.1e-24, TR:AAF18566 (EMBL:AF043232)
                     glycerol-3-phosphate phosphatase from Emericella nidulans
                     (Aspergillus nidulans) (236 aa) fasta scores; opt:  352,
                     z-score: 390.2, E(): 2.9e-14, 31.8% identity in 233 aa
                     overlap. Contains Pfam match to entry PF00702 Hydrolase,
                     haloacid dehalogenase-like hydrolase and Prosite match to
                     PS01228 Hypothetical cof family signature 1."
                     /codon_start=1
                     /transl_table=11
                     /product="putative hydrolase"
                     /protein_id="CAB92822.1"
                     /db_xref="GI:8246787"
                     /translation="MTATASTVLPARALLLDMDGTLVNSDAAVDRVWRRWADRHGLDG
                     DEVMKVVHGRQGYASMALLLPDRPMEHNHADNARMLAEETADTEGVVAIPGAAEFLAS
                     LRGLPHALVTSADVALSTARMAAAGLAQPDVRVTAESVGASKPDPEGFLKGAAELGIA
                     PADCVVFEDSGAGIAAGRAAGMRVVGVGPRAGFHGPDVVVEDLTRVRVEADADGGLRL
                     HIG"
     misc_feature    complement(4365. .4904)
                     /gene="SCC8A.04c"
                     /note="Pfam match to entry PF00702 Hydrolase, haloacid
                     dehalogenase-like hydrolase, score 135.50, E-value
                     9.9e-37"
     misc_feature    complement(4863. .4898)
                     /gene="SCC8A.04c"
                     /note="PS01228 Hypothetical cof family signature 1"

  Query Match             91.6%;  Score 17.4;  DB 3;  Length 32274;
  Best Local Similarity   94.7%;  Pred. No. 4.4e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           ||||||||||||||||| |||
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Db 24795 GCGCTCGGCCTGGTCGCGG 24777

RESULT 7
AC007207/c
LOCUS AC007207 191877 bp DNA PRI 23-NOV-1999
DEFINITION Homo sapiens 12p13.3-4.6-10.5 BAC RP11-320N7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
ACCESSION AC007207
VERSION AC007207.22 GI:6466489
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 191877)
AUTHORS Muzny,D.M., Adams,C., Bailey,M., Barbaria,J., Blankenburg,K., Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C., Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C., David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N., Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,L.L., Guevara,W., Harris,K., Hernandez,J., Hodgson,A., Hogues,M., Holloway,C., Hosak,H., Issar,A., Jackson,L.E., Jackson,L., Jia,Y., Jones,M., Kelly,S., Kneitz,S., Kondejewski,N., Kong,Y., Kovar,C., Lau,S., Leal,B., Lee,E., Li,Z., Lichtarge,O., Liu,J., Liu,W., Logan,O., Lu,J., Lucier,R., Marondel,I., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Merscher,S., Miller,A., Montgomery,K.T., Morgan,M., Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S., Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L., Quiles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S., Shah,E., Shen,H., Shim,C., Simon,M., Sparks,A., Stamps,A., Sucgang,R., Tabor,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wahbah,M., Watlington,S., Weinstock,G., Weinstock,I.R., Williamson,A., Worley,K., Wren,J., Wrensford,G., Xhang,A.M., Yang,R., Yu,W., Zhou,X., Kucherlapati,R., Nelson,D. and Gibbs,R.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 191877)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1999) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 191877)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (23-NOV-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Nov 23, 1999 this sequence version replaced gi:6091647.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT.

FEATURES Location/Qualifiers
source 1. .191877
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12p13.3"
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  Query Match             91.6%;  Score 17.4;  DB 86;  Length 191877;
  Best Local Similarity   94.7%;  Pred. No. 2.2e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
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Db   12728 GCGCTCGGCCTGGGCCCGG 12710


RESULT   8
AC084375
LOCUS       AC084375   201290 bp    DNA             HTG       19-NOV-2000
DEFINITION  Homo sapiens chromosome 12p clone RP11-664D1, WORKING DRAFT
            SEQUENCE, 6 unordered pieces.
ACCESSION   AC084375
VERSION     AC084375.4  GI:11225345
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 201290)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
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            Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
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            Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
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            and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 201290)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-OCT-2000) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 18, 2000 this sequence version replaced gi:11192103.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: HMGI
                Center clone name: RP11-664D1
            -------------- Summary Statistics
                Sequencing vector: M13; L08821
                Chemistry: Dye-primer Bodipy: 5% of reads
                Chemistry: Dye-terminator Big Dye: 95% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 195975 bases at least Q40
                Consensus quality: 199362 bases at least Q30
                Consensus quality: 200461 bases at least Q20
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            Estimated insert size: 198628; sum-of-contigs estimation
            Quality coverage: 0x in Q20 bases; agarose-fp estimation
            Quality coverage: 6.5x in Q20 bases; sum-of-contigs estimation
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          * NOTE: Estimated insert size may differ from sequence length
          *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 6 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *       1    79976: contig of 79976 bp in length
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          *  155733   155832: gap of unknown length
          *  155833   180188: contig of 24356 bp in length
          *  180189   180288: gap of unknown length
          *  180289   190769: contig of 10481 bp in length
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          *  200073   200172: gap of unknown length
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BASE COUNT    57512 a  44184 c  43798 g  55259 t    537 others
ORIGIN


  Query Match             91.6%;  Score 17.4;  DB 77;  Length 201290;
  Best Local Similarity   94.7%;  Pred. No. 2.2e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           ||||||||||||| |||||
Db  120723 GCGCTCGGCCTGGGCCCGG 120741


RESULT   9
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LOCUS       AC005842   300691 bp    DNA             HTG       11-NOV-2000.
DEFINITION  Homo sapiens clone RP11-303E5, WORKING DRAFT SEQUENCE, 20 unordered
            pieces.
ACCESSION   AC005842
VERSION     AC005842.11  GI:11136692
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 300691)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
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            and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 300691)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-1998) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 10, 2000 this sequence version replaced gi:11094657.
            ---------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            ---------- Project Information
                Center project name: YO
                Center clone name: RP11-303E5
            ---------- Summary Statistics
                Sequencing vector: Plasmid; M77789
                Sequencing vector: M13; L08821
                Chemistry: Dye-primer Bodipy: 2% of reads
                Chemistry: Dye-terminator Big Dye: 46% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 288810 bases at least Q40
                Consensus quality: 293327 bases at least Q30
                Consensus quality: 295549 bases at least Q20
                Estimated insert size: 290790; sum-of-contigs estimation
                Quality coverage: 11.9x in Q20 bases; sum-of-contigs estimation
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            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
            * NOTE: This sequence may represent more than one clone.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 20 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *  173518   173617: gap of unknown length
            *  173618   186953: contig of 13336 bp in length
            *  186954   187053: gap of unknown length
            *  187054   201262: contig of 14209 bp in length
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            *  201363   212476: contig of 11114 bp in length
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            *   212477   212576: gap of unknown length
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            *   247121   247220: gap of unknown length
            *   247221   261011: contig of 13791 bp in length
            *   261012   261111: gap of unknown length
            *   261112   272260: contig of 11149 bp in length
            *   272261   272360: gap of unknown length
            *   272361   278249: contig of 5889 bp in length
            *   278250   278349: gap of unknown length
            *   278350   282170: contig of 3821 bp in length
            *   282171   282270: gap of unknown length
            *   282271   287119: contig of 4849 bp in length
            *   287120   287219: gap of unknown length
            *   287220   291298: contig of 4079 bp in length
            *   291299   291398: gap of unknown length
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            *   296709   298055: contig of 1347 bp in length
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            *   299354   299453: gap of unknown length
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FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="RP11-303E5"
BASE COUNT    83346 a  63543 c  63933 g  87891 t   1978 others
ORIGIN


  Query Match             91.6%;  Score 17.4;  DB 60;  Length 300691;
  Best Local Similarity   94.7%;  Pred. No. 1.9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
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Db  45619 GCGCTCGGCCTGGGCCCGG 45601


RESULT  10
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LOCUS       BPD3112AB    2963 bp    DNA             PHG       11-APR-1996
DEFINITION  Bacteriophage D3112 A and B genes.
ACCESSION   X87627
VERSION     X87627.1  GI:974768
KEYWORDS    B protein; transposase.
SOURCE      Bacteriophage D3112.
  ORGANISM  Bacteriophage D3112
            Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
            Lambda phage group.
REFERENCE   1  (bases 1 to 2963)
  AUTHORS   Ulycznyj,P.I., Salmon,K.A., Douillard,H. and DuBow,M.S.
  TITLE     Characterization of the Pseudomonas aeruginosa transposable
            bacteriophage D3112 A and B genes
  JOURNAL   Biochim. Biophys. Acta 1264 (3), 249-253 (1995)
  MEDLINE   96138540
REFERENCE   2  (bases 1 to 2963)
  AUTHORS   Ulycznyj,P.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAY-1995) P.I. Ulycznyj, McGill University, Dept of
            Microbiology & Immunology, 3775 University St., Montreal, Quebec
            H3A 2B4, CANADA
FEATURES             Location/Qualifiers
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                     /strain="cts15"
                     /db_xref="taxon:10708"
                     /map="2521-5483bp"
     gene            8. .2091
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                     DQAERGALVPKVRRPDMSVPDWAPAFMTIYQGPEKRSARAAHALLEKHWQGQMPSLDQ
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                     HGRPFRPEITTIIDIRTRRIPGWSTGLAESALVVVDALRDACIKGGVPAIFYVDNGSG
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                     DRQAKLATFKLTRRAIAKGGTMPLMSWESFVAFCEQQIAEYNDRPHSSLPRIVDPNTG
                     RRRHMTPNEAWALHEAEGFSPMRVTDDEARPLFRPQVLRTVRRCELEFIGNRYFAREL
                     EEFHGDQVAVGYDIHDASRVWVYDGEGRFLCTAELNGNSRDYMPASYVERAREKRAEA
                     REKRALAHLDEIRAERDGGYALEMDAPLSIPGLGTITPEQLRSRSAATLEVQAERIDE
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                     ELAASGRPLIIDEMDHLVAAGQVELIRDLYESSQASILLIGEEMLPTKLKKFERFHGR
                     VLSWVPAQPVSLEDARNLAPVYSPGVAIADDLLAHLVKKSLGSVRRVAVNLEQLAEAA
                     TVQGRRDVELADLQRLNLELYTGAAPSPRTSK"
BASE COUNT      558 a   1033 c    927 g    445 t
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 11;  Length 2963;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CGCTCGGCCTGGTCCCGG 19
          |||||||||||||| ||
Db    512 CGCTCGGCCTGGTCCAGG 495


RESULT  11
AF099190/c
LOCUS       AF099190     3611 bp    DNA             BCT       10-NOV-1999
DEFINITION  Caulobacter crescentus penicillin binding protein B (divA) gene,
            complete cds; and unknown genes.
ACCESSION   AF099190
VERSION     AF099190.1  GI:6318312
KEYWORDS    .
SOURCE      Caulobacter crescentus.
  ORGANISM  Caulobacter crescentus
            Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
            Caulobacter.
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REFERENCE   1  (bases 1 to 3611)
  AUTHORS   Ohta,N. and Newton,A.
  TITLE     The divA gene product, penicillin binding protein B, is required
            for the initiation step of cell division in Caulobacter
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3611)
  AUTHORS   Ohta,N. and Newton,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1998) Molecular Biology, Princeton University,
            Washington Rd., Princeton, NJ 08544, USA
FEATURES             Location/Qualifiers
     source          1. .3611
                     /organism="Caulobacter crescentus"
                     /strain="CB15"
                     /db_xref="taxon:76"
                     /note="complements cell division defect of divA305
                     mutation"
     CDS             <1. .411
                     /note="OrfC"
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                     /protein_id="AAF06833.1"
                     /db_xref="GI:6318313"
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                     RRREERPFERTLDLAEVIERAVGGRKGAKVHPATRSFQGLRIAVNDELGELEAGLAAA
                     ERVLKPGGRLVVVTFHSLEDRIVKAFLAERAGKAPGGSRHAPPVAAGAAPSFQLISNK
                     AIAPSEAELAVNPRARSSKLRAAVRTDAPVWEAAG"
     CDS             1340. .1783
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                     /protein_id="AAF06836.1"
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                     IFNLGLPGVTFEEQERRMYPLGPTAAHLIGFVDSGGKGLAGAERALDDPIRKAAGGEG
                     GPAQLSIDVRVQAALEDELRKAAEEFTPKGAVGLVTNVHTGEILGMASWPDYDANKAG
                     GATDDQRLNRAAASVYEMGSTFKAFTVAIGLDTGVATAASTFDAREPYKLGYRTIHDY
                     HATKAVLNLVEVFQHSSNIGTAMLAERVGGQRLSQYFTNLGLTKPAKVELQESARPLT
                     PRKWDQDTVASTSFGHGMNISPLALAQAMNALLNGGEMRPLTIRKLPPGVRPEGRRVL
                     SEHTSAEMLKIMRANVVPGEGGSGGKADVPGLSVGGKTGTGEKYDPAIRRYNHQRQVS
                     SFAATFPTDGPLEADRYFVLILLDEPKGNANSFGFSTGGWVAAPAAGRVIERIAPFLG
                     VKRKTELVTIANSPKNAAPEAGL"
BASE COUNT      533 a   1237 c   1265 g    576 t
ORIGIN
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  Query Match           86.3%;  Score 16.4;  DB 1;  Length 3611;
  Best Local Similarity  94.4%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCG 18
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Db    725 GCGCTCGGCCTGGTCCAG 708


RESULT  12
U18133/c
LOCUS       U18133       4988 bp    DNA             BCT       15-AUG-2000
DEFINITION  Comamonas testosteroni BR60 CbaR (cbaR),
            3-chlorobenzoate-3,4/4,5-dioxygenase (cbaA),
            3-chlorobenzoate-3,4/4,5-dioxygenase reductase (cbaB), and
            1-carboxy-3-chloro-3,4-dihydroxycyclohexa-1,5-diene dehydrogenase
            (cbaC) genes, complete cds.
ACCESSION   U18133 U00692
VERSION     U18133.2  GI:9820075
KEYWORDS    .
SOURCE      Comamonas testosteroni.
  ORGANISM  Comamonas testosteroni
            Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
            Comamonas.
REFERENCE   1  (bases 1 to 4988)
  AUTHORS   Nakatsu,C., Ng,J., Singh,R., Straus,N. and Wyndham,C.
  TITLE     Chlorobenzoate catabolic transposon Tn5271 is a composite class I
            element with flanking class II insertion sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88 (19), 8312-8316 (1991)
  MEDLINE   92020843
REFERENCE   2  (bases 1 to 4988)
  AUTHORS   Nakatsu,C.H., Straus,N.A. and Wyndham,R.C.
  TITLE     The nucleotide sequence of the Tn5271 3-chlorobenzoate
            3,4-dioxygenase genes (cbaAB) unites the class IA oxygenases in a
            single lineage
  JOURNAL   Microbiology 141 (Pt 2), 485-495 (1995)
  MEDLINE   95219104
REFERENCE   3  (bases 1 to 4988)
  AUTHORS   Nakatsu,C.H., Providenti,M. and Wyndham,R.C.
  TITLE     The cis-diol dehydrogenase cbaC gene of Tn5271 is required for
            growth on 3-chlorobenzoate but not 3,4-dichlorobenzoate
  JOURNAL   Gene 196 (1-2), 209-218 (1997)
  MEDLINE   97464069
REFERENCE   4  (bases 1 to 4988)
  AUTHORS   Providenti,M.A. and Wyndham,R.C.
  TITLE     Identification of CbaR, a MarR-family modulator of cbaABC, the
            3-chlorobenzoate catabolic operon of Tn5271
  JOURNAL   Unpublished
REFERENCE   5  (bases 1244 to 4988)
  AUTHORS   Wyndham,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1993) Campbell Wyndham, Carleton University,
            Institute of Biology, 1125 Colonel By Drive, Ottawa, Ontario, K1S
            5B6, Canada
REFERENCE   6  (bases 1 to 4988)
  AUTHORS   Wyndham,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-APR-2000) Campbell Wyndham, Carleton University,
            Institute of Biology, 1125 Colonel By Drive, Ottawa, Ontario, K1S
            5B6, Canada
  REMARK    Sequence update by submitter
COMMENT     On Aug 15, 2000 this sequence version replaced gi:2073549.
FEATURES             Location/Qualifiers
     source          1. .4988
                     /organism="Comamonas testosteroni"
                     /transposon="Tn5271"
                     /strain="BR60"
                     /isolate="Bloody Run Creek"
                     /db_xref="taxon:285"
                     /clone="pBRH2"
                     /plasmid="pBRC60"
     gene            complement(239. .760)
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                YVKAHWHRESPQE"
     -10_signal 1319. .1324
     mRNA       1331. .2727
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                /product="CbaA"
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                /gene="cbaA"
     RBS        1418. .1422
                /gene="cbaA"
                /note="putative"
     CDS        1429. .2727
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                /note="CbaA"
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                /transl_table=11
                /evidence=experimental
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                DMPSVRPEDEFKNSVRVARYPVKEMAGVVWVYMGTRKVLPELPRLEVLNLPENEVDVI
                CLQRKSNWLQNLEGEIDTSHFNFLHVGGLHADEVPDDHPLKYTAQVAPQYLVKETALG
                TCYAAQVPAEEDHTYTRFAHFLFPFWALIPQADIAQNILARAWVPMDDEHTMMFFFRW
                TGSKAKRLDTPLKSGSPMPGVTLTDMKYKENTTDWYGRWQPLGDESNDWLIDRDLQKV
                GRVFSGIYGIHAQDQAMTDSMGPIIDHGLEQLAPTDLMIVRTRRRILKALRAHEANGT
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                /evidence=experimental
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                RNAFALDPQARETVLICGGIGITPMVHMAMTLVKAKRPWSMHIASRDGDELDLLGPLG
                SCSEISRYISSQGDRLPIRDLAERAPANAHLYFCGPEGMLQEFLAATQHRDPATVHYE
                QFQAAPSTGNEFTVNLARSGAQYVVREGETILDVLRNAGHHVTSSCRQGICGMCETTL
                ISGVPDHRDRLLTDSEKASGRTMLICCSRALSPELTLDL"
     gene       3731. .4924
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                /evidence=experimental
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                /db_xref="GI:2073552"
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                AEELNTDLGGGVVFNQASHQLDVIRLLAQGRVVDVSSYLGRWDAARRTEGAYSALIKF
                DNGVAANVTYSGYAHYNSDEVMGWVNELGEKQPERRLFPTRLRLDEVLNKGSEAAYKN
                EMSYGRGWSAHGLPKMARNHQHFGHLVISCEGADIVPKAEKIEVFANGEYHCENFSMP
                DFPRQEVMDELFDAISGTRPPVHTGEWAMETLDLCIALLEGGKPELIGMRATAVACAG
                RSSGR"
BASE COUNT     1005 a   1422 c   1535 g   1026 t
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 3;  Length 4988;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCG 18
           |||||||||| |||||||
Db    3332 GCGCTCGGCCAGGTCCCG 3315


RESULT  13
AF319543
LOCUS       AF319543     6927 bp    DNA             BCT       11-JAN-2001
DEFINITION  Streptomyces venezuelae putative acetyl-CoA acetyltransferase and
            cystathionine beta-synthase (CbsSV) genes, complete cds.
ACCESSION   AF319543
VERSION     AF319543.1  GI:12082814
KEYWORDS    .
SOURCE      Streptomyces venezuelae.
  ORGANISM  Streptomyces venezuelae
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE   1  (bases 1 to 6927)
  AUTHORS   Chang,Z.
  TITLE     Genes for cysteine biosynthesis and metabolism in Streptomyces
            venezuelae ISP5230: cloning, sequencing, functional analysis and
            relevance to chloramphenicol biosynthesis
  JOURNAL   Thesis (1999) Dalhousie University, Biology, Halifax, NS, Canada
REFERENCE   2  (bases 1 to 6927)
  AUTHORS   Chang,Z. and Vining,L.C.
  TITLE     Cystathionine beta-synthase in Streptomyces venezuelae ISP5230: an
            alternative pathway of cysteine biosynthesis
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 6927)
  AUTHORS   Chang,Z. and Vining,L.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2000) Biology, Dalhousie University, Halifax, NS
            B3H 4J1, Canada
FEATURES             Location/Qualifiers
     source          1. .6927
                     /organism="Streptomyces venezuelae"
                     /strain="ISP5230"
                     /db_xref="taxon:54571"
     CDS             complement(1974. .3194)
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                     /protein_id="AAG48622.1"
                     /db_xref="GI:12082816"
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                     REDGLVPDAYIAMGQTAENLARWKGITRQEMDEFGVRSQNLAEQAIKNGFWEREITPV
                     TLPDGTVVSTDDGPRAGVTLEGVSGLKPVFRPDGLVTAGNCCPLNHGAAALVIMSDTK
                     ARELGLTPLARIVSTGVSGLSPEIMGLGPVEASKQALQRAGLTIGDIDLAEINEAFAA
                     QVIPSYQELGLDLDKVNVNGGAIAVGHPFGMTGARITGTLINSLQFHDKQFGLETMCV
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     gene            4460. .5851
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                     /function="catalyses the formation of cystathionine from
                     homocysteine and serine"
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                     /transl_table=11
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                     /db_xref="GI:12082815"
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                     INVLRAYGAEVVVCPTAVDPEHPDSYYNVSDRLVRETPGAWKPDQYSNPNNPRSHYET
                     TGPELWEQTDGKITHFVAGVGTGGTISGTGNYLKEASGGSVKIIGADPEGSVYSGGSG
                     RPYLVEGVGEDFWPTAYDRNVTDRIVAVSDKDSFQMTRRLAKEEGLLVGGSCGMAVVA
                     ALEVARELGPDDVVVVLLPDSGRGYMSKIFSDEWMAGHGFLEDTSSATVADVLRHKEG
                     GTMPSLVHMHPDETVGQAIEVLREYGVSQMPIVKPGAGHPDVMAAEVVGSVVERDVLD
                     ALFTQRASLEDSLESHMSAPLPQVGSGEPVAALMSVLGDAADAAIVLVEGKPTGVVSR
                     QDLLAFLANGGAK"
BASE COUNT      945 a    2483 c    2539 g     960 t
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 2;  Length 6927;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CGCTCGGCCTGGTCCCGG 19
           |||||||||||||| ||
Db    6273 CGCTCGGCCTGGTCCAGG 6290


RESULT  14
SCARGGH
LOCUS       SCARGGH      8300 bp    DNA             BCT       23-MAR-2000
DEFINITION  Streptomyces clavuligerus arginine biosynthesis cluster (argCJBDRGH
            genes).
ACCESSION   Z49111 M83659 Y11134
VERSION     Z49111.2  GI:7328261
KEYWORDS    acetylglutamate kinase; acetylornithine aminotransferas; argB gene;
            argC gene; argD gene; argG gene; argH gene; arginine regulator;
            argininosuccinate lyase; argininosuccinate synthetase; argJ gene;
            argR gene; glutamate N-acetyltransferase;
            N-acetyl-gamma-glutamyl-phosphate reductase.
SOURCE      Streptomyces clavuligerus.
  ORGANISM  Streptomyces clavuligerus
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; .
            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE   1  (bases 1 to 8300)
  AUTHORS   Ludovice,M., Martin,J.F., Carrachas,P. and Liras,P.
  TITLE     Characterization of the Streptomyces clavuligerus argC gene
            encoding N-acetylglutamyl-phosphate reductase: expression in
            Streptomyces lividans and effect on clavulanic acid production
  JOURNAL   J. Bacteriol. 174 (14), 4606-4613 (1992)
  MEDLINE   92325051
REFERENCE   2  (bases 1 to 8300)
  AUTHORS   Rodriguez-Garcia,A., Martin,J.F. and Liras,P.
  TITLE     The argG gene of Streptomyces clavuligerus has low homology to
            unstable argG from other actinomycetes: effect of amplification on
            clavulanic acid biosynthesis
  JOURNAL   Gene 167 (1-2), 9-15 (1995)
  MEDLINE   96144242
  REMARK    (sites)
REFERENCE   3  (bases 1 to 8300)
  AUTHORS   Rodriguez-Garcia,A., Ludovice,M., Martin,J.F. and Liras,P.
  TITLE     Arginine boxes and the argR gene in Streptomyces clavuligerus:
            evidence for a clear regulation of the arginine pathway
  JOURNAL   Mol. Microbiol. 25 (2), 219-228 (1997)
  MEDLINE   97426030
REFERENCE   4  (bases 1 to 8300)
  AUTHORS   Rodriguez-Garcia,A., de la Fuente,A., Perez-Redondo,R., Martin,J.F.
            and Liras,P.
  TITLE     Characterization and expression of the arginine biosynthesis gene
            cluster of Streptomyces clavuligerus
  JOURNAL   Unpublished
REFERENCE   5  (bases 1 to 8300)
  AUTHORS   Rodriguez-Garcia,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-1995) Rodriguez-Garcia A., Universidad de Leon,
            Facultad de Biologia, Area de Microbiologia, Campus de Vegazana,
            Leon, Spain, 24071
  REMARK    Revised by [6]
REFERENCE   6  (bases 1 to 8300)
  AUTHORS   Rodriguez-Garcia,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-2000) Rodriguez-Garcia A., Area de Microbiologia,
            Universidad de Leon, Facultad de Biologia, Leon, 24071, SPAIN
COMMENT     On Apr 11, 2000 this sequence version replaced gi:153165 gi:1839024
            gi:886905.
FEATURES             Location/Qualifiers
     source          1. .8300
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                     /strain="ATCC 27064"
                     /db_xref="taxon:1901"
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                     /citation=[1]
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                WSVGGMAKGAGMLAPGLATLLVVLTTDADLAPPVLDKAVRDAVRTTFERVDSDGCMST
                NDTVLLLASGASGGDPGYEEFADVLREVCEDLARKLIGDAEGASKDIRIEVIHAATED
                DAVEVGRTIARNNLLKCAIHGEDPNWGRVLSAIGTTKAVFEPERLNVAINGVWVCREG
                SAGDGRDLVDMRFREVRITADLDAGTHSAVIWANDLTAEYVHENSAYSS"
     gene       2423. .2451
                /gene="argB"
     repeat_region 2423. .2451
                /gene="argB"
                /citation=[4]
                /rpt_unit=2423. .2433
                /rpt_type=DIRECT
     gene       join(2474. .2478,2485. .3393)
                /gene="argB"
     RBS        2474. .2478
                /gene="argB"
     CDS        2485. .3393
                /gene="argB"
                /EC_number="2.7.2.8"
                /function="arginine biosynthesis"
                /citation=[4]
                /codon_start=1
                /transl_table=11
                /evidence=experimental
                /product="acetylglutamate kinase"
                /protein_id="CAB82481.1"
                /db_xref="GI:7328264"
                /translation="MTRKNNALPKARTLIEALPWLTRHHGKTIVVKFGGNAMVNEELK
                GAFARPSFLVHHAGLRPVVVHGGGPQISAELDRYGLVSEFKAGLRVTTDEAMDVVRMV
                LAGQVQRDVWGCSIVHGPLAVGITGEDAHPISATRHRPLIDGEPVDIGRVGEVTRIDT
                GAVLALLEDGRIPVVSSIARAEDDGHVYNVNADTAAAALAAALGAETLMVLTDVEGLY
                EDWPNSDEVISRLTASELETLLPDLSSGMVPKMEGCLHAVRNGVRTARVIDGRVPHSI
                LLEIFTDDGVGTMVVPDEPSVSEGTS"
     gene       3379. .3382
                /gene="argD"
     RBS        3379. .3382
                /gene="argD"
     gene       3390. .4592
                /gene="argD"
     CDS        3390. .4592
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                /EC_number="2.6.1.11"
                /function="arginine biosynthesis"
                /citation=[4]
                /codon_start=1
                /transl_table=11
                /evidence=experimental
                /product="acetylornithine aminotransferase"
                /protein_id="CAB82482.1"
                /db_xref="GI:7328265"
                /translation="MSNQEFAQRWQGVMIDSYGTPGLSFVRGEGSTLWDADGTAYTDF
                VSGLAVNALGHAHPAVVGAVSRQIASLGHISNFYSAEPTITLAERLIELFGRPGRVFF
                CNSGAEANETAFKIGRLTGRSRIVAAQSGFHGRTMGSLALTGQPAKREPFLPLPGDVT
                HVPYGDAEALRAAVTEDTAMVILEPIQGESGVVVPPKGYLRAAREITEATGTLLVLDE
                VQTGIGRTGHWFAAQAEGVEADVVTLAKGLGGGLPLGAAVAFGRAAELMTPGHHASTF
                GGNPVSCARTRVLDTIAADGLLDRVKQLGSAPDEWSVRDAAAIRWSPMSGAGLMLGIV
                LNEPLAPQVQLAAQKAGFLVNVPAPDVVRLIPPLVIEETEVDAFLQALPGLLDAVHER
                DREGQTGE"
```

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     gene       4594. .5136
                /gene="argR"
     misc_feature 4594
                /gene="argR"
                /note="Transcription start point"
                /citation=[4]
                /evidence=experimental
     CDS        4600. .5136
                /gene="argR"
                /function="arginine metabolism regulation"
                /citation=[3]
                /codon_start=1

  Query Match             86.3%;  Score 16.4;  DB 3;  Length 8300;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CGCTCGGCCTGGTCCCGG 19
          ||||||||||| |||||
Db   7320 CGCTCGGCCTGGACCCGG 7337


RESULT  15
SC5H1
LOCUS       SC5H1       36583 bp    DNA             BCT       06-JUN-2000
DEFINITION  Streptomyces coelicolor cosmid 5H1.
ACCESSION   AL049863
VERSION     AL049863.2  GI:8347022
KEYWORDS    add; adenosine deaminase; ATP-dependent Clp protease; bldA codon;
            chiF; chitinase; clpP3; clpP4; DNA-binding protein; hydroxylase;
            ion channel subunit; isomerase; myo-inositol dehydrogenase;
            oxidoreductase; protease; ribonuclease H; RNA polymerase sigma
            factor; rnhA; serine/threonine protein kinase; transcriptional
            regulator.
SOURCE      Streptomyces coelicolor A3(2).
  ORGANISM  Streptomyces coelicolor A3(2)
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE   1  (bases 1 to 36583)
  AUTHORS   Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
            Kinashi,H. and Hopwood,D.A.
  TITLE     A set of ordered cosmids and a detailed genetic and physical map
            for the 8 Mb Streptomyces coelicolor A3(2) chromosome
  JOURNAL   Mol. Microbiol. 21 (1), 77-96 (1996)
  MEDLINE   97000351
REFERENCE   2  (bases 1 to 36583)
  AUTHORS   Oliver,K. and Harris,D.
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 36583)
  AUTHORS   James,K.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-1999) Streptomyces coelicolor sequencing project,
            Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
            CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
            David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
            Colney, Norwich, Norfolk NR4 7UH, UK
COMMENT     On Jun 8, 2000 this sequence version replaced gi:4835303.
            Notes:
            Streptomyces coelicolor sequencing at The Sanger Centre is funded
            by the BBSRC.
            Details of S. coelicolor sequencing at the Sanger Centre are
            available on the World Wide Web.
            (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
            CDS are numbered using the following system eg SC7B7.01c. SC (S.
            coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
            strand).
            The more significant matches with motifs in the PROSITE database
            are also included but some of these may be fortuitous.
            The length in codons is given for each CDS.
            Usually the highest scoring match found by fasta -o is given for
            CDS which show significant similarity to other CDS in the database.
            The position of possible ribosome binding site sequences are given
            where these have been used to deduce the initiation codon.
```

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
Cosmid 5H1 lies between 2G2 and 5F8 on the AseI-A genomic restriction fragment.

FEATURES Location/Qualifiers

source 1. .36583
/organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
/db_xref="taxon:100226"
/clone="cosmid 5H1"

repeat_unit complement(179. .238)
/note="55 bp imperfect inverted repeat"

gene complement(209. .1246)
/gene="SC5H1.41"

CDS complement(209. .1246)
/gene="SC5H1.41"
/note="SC5H1.41, hypothetical protein, len: 345 aa; unknown function, similar to part of SCE29.03 (EMBL:AL035707) S.coelicolor putative phosphotransferase (300 aa), fasta scores; opt: 433 z-score: 437.4 E(): 4.9e-17, 37.2% identity in 269 aa overlap. Contains TTA (leucine) codon, possible target for bldA regulation. There are imperfect inverted repeats at each end of the CDS"
/codon_start=1
/transl_table=11
/label=SC5H1.41
/product="hypothetical protein"
/protein_id="CAB42966.1"
/db_xref="GI:4835344"
/db_xref="SPTREMBL:Q9X7U8"
/translation="MLGAGRARLGAGPGTQPLSGRIDLSGPQGAQLRTAIAAVHRICP
EFSPVQVLRRSGRSVLLVGTTGRSTAVAKCLVDHSPAWAERSRHEIGAYRSFVRQRPP
VRVPRLIAADPDNGTLVIERMPGRVAALQRHPLEAPPRADIRAAIGAVCRLNAWRPPA
GTFDAPLDYAARISRYHELGLLTDRDLGDLQKLLHGIAHAGGRQGMGQFCHGDALLSN
VLMSPAGPVLVDWEHAGWYLPGYDLATLWAVLGDAPVARRQISQIAQSTGTAARDAFL
VNLMLVLTREIRTYETAVQRSMHDPVGAATGPAHPGAAPTGEEQRLLLRRLHDDCQLA
RRAVRAAVGTR"

misc_feature complement(1022. .1024)
/gene="SC5H1.41"
/note="TTA (leucine) codon, possible target for bldA regulation"

repeat_unit complement(1287. .1346)
/note="55 bp imperfect inverted repeat"

gene 1648. .3156
/gene="SC5H1.40c"

CDS 1648. .3156
/gene="SC5H1.40c"
/note="SC5H1.40c, possible regulatory protein, len: 502 aa; similar to e.g. SW:SP15_STRGR (EMBL:M32687) Streptomyces griseus sporulation protein (529 aa), fasta scores; opt: 394 z-score: 452.2 E(): 7.2e-18, 27.9% identity in 530 aa. Similar to SC7A1.26 (EMBL:AL034447) S.coelicolor possible transcriptional regulator (500 aa) (43.0% identity in 491 aa overlap)"
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/transl_table=11
/label=SC5H1.40c
/product="putative regulatory protein"
/protein_id="CAB42965.1"
/db_xref="GI:4835343"
/db_xref="SPTREMBL:Q9X7U7"
/translation="MSKEPNTRLSDLFGLAGWSKGELARLVNRQAAAMGHPQLATDTS
RVRRWIDMGEIPRDPVPRVLAALFTERLGRVVTIEDLGLVRHGRAGKRPHDGSEEHPD
GVPWAPERTAAVLTEFTGMDLMLNRRGLVGAGAALAAGSALSSAMHDWLHTDPALAAD
APDLHQPLHADPAGFDRYEAAPIGSQEVEELERSVEVFRAWDAARGGGLQRKAVVGQL
NEVGGMLAYHHPPHLQRRLWGVAANLAVLAGWMSHDVGLEPTAQKYFVIAAHAAREGG
DRPRAGEALSRAARQMVHLGKPDEALDLMKLAQSGSGEQVLPRTKAMLYTIEAWAQAS
MGKGQAMRRTLGRAEDLFVSDKADVPPPDWMQTFKEEDLYGMQALAYRTLAEFEPGAA
AHAQHYADKALALRIDGRQRSKIFDYLSMASACFIADDPEQADRYARLALVSMGSNSS
QRTWDRLRQMYRLTAEYAGYPKIQELREEIKLALPKGKSPRGKGPGGTVAPA"

gene complement(3176. .4492)
/gene="SC5H1.39"

CDS complement(3176. .4492)
/gene="SC5H1.39"
/note="SC5H1.39, hypothetical protein, len: 438 aa; unknown function, probable CDS suggested by positional base preference, GC frame analysis and amino acid composition"
/codon_start=1
/transl_table=11
/label=SC5H1.39
/product="hypothetical protein"
/protein_id="CAB42964.1"
/db_xref="GI:4835342"
/db_xref="SPTREMBL:Q9X7U6"
/translation="MSSHLSADHPAAQSPGQGSVEALISQTRRLRGDVDAVRRDSQDD
TTDPRGRWQRALYDLALHQLTDLDAHLAQLRDGPAPAPRAGSLLSRVGSAEWNLLTDE
AEWSAELFHILGRDPASVPLSLDELPSLVLTEDRPKLTAMVTDCLVDGRPIDGEFRVV
RPDGSVRTVHMMGEPVLDADGSTASMWAVLRDVGELRRSQRAVSETRDSLRRRPASPW
HGLLRFPDEGRPGLDLAGAHLPPTSATGRRSREGGWYDACPLGADGETLITVGDFGLP
EADAYGPAVLIGALRGLALAGTRPGRLRDRLAELLRATALAPVDGAVYCGYRPDTHTL
TWAHASGPAPLLFRGGTGHALSGPDGPAGQDGPSGEAEATLEAGDLLLLHTGALEPEA
VEHLLTLAPRLTAADSAGDGVRLVTRELDGFPGRQDACVLIARVTP"

gene complement(4765. .5793)
/gene="SC5H1.38"

CDS complement(4765. .5793)
/gene="SC5H1.38"
/note="SC5H1.38, probable myo-inositol dehydrogenase, len: 342 aa; similar to many e.g. SW:MI2D_BACSU (EMBL:M76431), idh, Bacillus subtilis myo-inositol 2-dehydrogenase (344 aa), fasta scores; opt: 864 z-score: 958.5 E(): 0, 38.1% identity in 336 aa overlap. Also similar to SW:STRI_STRGR (EMBL:Y00459), strI, Streptomyces griseus streptomycin biosynthesis myo-inositol oxidoreductase (348 aa) (32.7% identity in 343 aa overlap). Weakly similar to TR:O69945 (EMBL:AL023862) S.coelicolor possible oxidoreductase (430 aa) (29.8% identity in 228 aa overlap). Contains Pfam match to entry PF01408 GFO_IDH_MocA, Oxidoreductase family, score 153.50, E-value 3.6e-42"
/codon_start=1
/transl_table=11
/label=SC5H1.38
/product="putative myo-inositol dehydrogenase"
/protein_id="CAB42963.1"
/db_xref="GI:4835341"
/db_xref="SPTREMBL:Q9X7U5"
/translation="MSELLGVAVLGAGHMGADHIRRVDQVVSGARVAAVADPDAERAK
EAVGGIGGTGRITVHTDVEAALDAPGVEAVLIASPGEAHEEALLAAFARGLPVLCEKP
MAPNSAGALRVVEAEARLGRRLAQIGFMRRYDAEYRQLKSLLDGGRLGRPLMLHCVHR
NVSSPPHFTSAMLINSSVSHEIDAARWLLGQELSAVTVLRPRPSAGAPEGLLDPQLVL
FETEGGAVVDVEVFVNCGFGYEVRCEAVCEAGSARIGAAHTMMVTAAGGAREEVPQDY
LVRFADAYDREVQSWVDATRRGLVTGPGTWDGYAAAAVAEAGVRALDTGVRTPVDMAP
RPSLHDRA"

misc_feature complement(5062. .5781)
/gene="SC5H1.38"
/note="Pfam match to entry PF01408 GFO_IDH_MocA, Oxidoreductase family, score 153.50, E-value 3.6e-42"

RBS complement(5804. .5808)
/note="possible RBS"

gene complement(5917. .7011)
/gene="SC5H1.37"

CDS complement(5917. .7011)

/gene="SC5H1.37"
/note="SC5H1.37, hypothetical protein, len: 364 aa;
unknown function, similar to TR:P73120 (EMBL:D90903)
Synechocystis sp. hypothetical protein (358 aa), fasta
scores; opt: 492 z-score: 559.6 E(): 7.6e-24, 31.6%

Query Match 86.3%; Score 16.4; DB 3; Length 36583;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 CGCTCGGCCTGGTCCCGG 19
           |||||| ||||||||||
Db    7826 CGCTCGACCTGGTCCCGG 7843
```

Search completed: April 20, 2001, 00:00:44
Job time: 9521 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:13:00 ; Search time 547.68 Seconds
(without alignments)
20.252 Million cell updates/sec

Title: US-09-016-464-20
Perfect score: 19
Sequence: 1 GCGCTCGGCCTGGTCCCGG 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0401:*
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14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	18	T76133	Human eosinophil p
2	19	100.0	19	20	X53932	Eosinophil peroxid
3	19	100.0	19	21	F19494	Human eosinophil p
4	19	100.0	19	21	A33372	Low adenosine anti
5	19	100.0	60	18	T76132	Human eosinophil p
6	19	100.0	60	20	X53942	Intercellular adhe
7	19	100.0	60	21	F19504	Human eosinophil p
8	19	100.0	60	21	A33382	Low adenosine anti
9	19	100.0	272	20	X54603	Eosinophil peroxid
10	19	100.0	272	21	F20172	Human low adenosin
11	19	100.0	272	21	A34050	Human adenosine re
c 12	19	100.0	2272	21	Z45456	Nucleotide sequenc
c 13	19	100.0	2558	21	F20923	Human eosinophil p
c 14	19	100.0	2558	21	A34801	Human adenosine re
15	19	100.0	6103	21	F21441	Human eosinophil p
c 16	19	100.0	6103	21	F21441	Human eosinophil p
17	19	100.0	7033	21	F20844	Human low adenosin
18	19	100.0	7033	21	A34722	Human adenosine re
19	19	100.0	7036	20	X55274	Human factor-relat
c 20	19	100.0	35384	21	F21436	Human enzyme-relat
21	19	100.0	114955	20	X53491	Human adenosine A1
22	19	100.0	209273	21	F21437	Human factor-relat
23	15.8	83.2	1185	19	V05039	Alcaligenes eutrop
24	15.8	83.2	1185	20	Z08784	A. eutrophus beta-
25	15.8	83.2	1185	21	A71692	A. eutrophus bktB
26	15.8	83.2	1251	21	C44041	Zea mays DNA fragm
27	15.8	83.2	1401	14	Q34556	cDNA encoding TIAR
c 28	15.8	83.2	3012	21	Z52054	Codon optimised Hu
29	15.8	83.2	4738	14	Q50997	Rat NMDA receptor
c 30	15.8	83.2	8908	21	Z52055	Packaging construc
31	15.8	83.2	9960	19	V58939	Mycobacterium smeg
32	15.8	83.2	29879	14	Q46806	eryA region of S.
33	15.8	83.2	35099	19	V27112	Adenovirus 17. Ma
34	15.4	81.1	1332	21	C55830	S. lavendulae MmcP
c 35	15.4	81.1	1776	21	A71636	Human aspartate pr
c 36	15.4	81.1	2094	21	A71623	Human aspartate pr
c 37	15.4	81.1	2575	20	Z10654	cDNA encoding a hu
38	15.4	81.1	3293	17	T05810	Human thyroid tran
39	15.4	81.1	4052	16	Q87791	S. lavendulae mrd
c 40	15.4	81.1	38734	20	Z32020	Human METH1 relate
c 41	15.4	81.1	38734	22	C90077	AL021529 cDNA clon
c 42	15.4	81.1	53500	21	C55842	Complete nucleotid
43	15	78.9	15	20	X54604	Eosinophil peroxid
44	15	78.9	15	21	F20173	Human eosinophil p
45	15	78.9	15	21	A34051	Human adenosine re

ALIGNMENTS

RESULT 1
T76133
ID T76133 standard; DNA; 19 BP.
XX
AC T76133;
XX
DT 12-SEP-1997 (first entry)
XX
DE Human eosinophil peroxidase antisense oligonucleotide HSEPAS1.
XX
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; ss.
XX
OS Synthetic.
XX
PN WO9640162-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09306.
XX
PR 07-JUN-1995; 95US-0474497.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Metzger WJ, Nyce JW;
XX
DR WPI; 1997-051871/05.
XX
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject
XX
PS Claim 5; Page 27; 71pp; English.

```
XX
CC   A method for treating airway disease in a subject has been produced,
CC   which involves the topical administration of an essentially adenosine
CC   free antisense oligonucleotide (ON) to the airway epithelium of the
CC   subject. The present sequence is an antisense oligonucleotide
CC   HSEPAS1 specific for the human eosinophil peroxidase. The method
CC   can be used to treat airway diseases such as cystic fibrosis, asthma,
CC   chronic obstructive pulmonary disease, bronchitis and other
CC   airway diseases characterised by an inflammatory response. By
CC   eliminating adenosine from the antisense ON, its liberation upon
CC   antisense degradation is prevented, thereby preventing adenosine-
CC   induced bronchoconstriction in patients with hyper-reactive airways.
XX
SQ   Sequence 19 BP; 0 A; 8 C; 8 G; 3 T; 0 other;


  Query Match             100.0%;  Score 19;  DB 18;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 9.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db      1 gcgctcggcctggtcccgg 19


RESULT   2
X53932
ID   X53932 standard; DNA; 19 BP.
XX
AC   X53932;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Eosinophil peroxidase antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 46; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (X52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences X55272-74. These multiple target
CC   oligonucleotides (specifically X55180-271) can be used for the antisense
CC   treatment of diseases and conditions. Typical diseases and conditions
CC   are those associated with impaired respiration and inflammation,
CC   including lung diseases, pulmonary vasoconstriction, inflammation,
CC   allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC   respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC   hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC   carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC   cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC   metastases, as well as all types of cancers which may metastasize or have
CC   metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 19 BP; 0 A; 8 C; 8 G; 3 T; 0 other;


  Query Match             100.0%;  Score 19;  DB 20;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 9.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db      1 gcgctcggcctggtcccgg 19


RESULT   3
F19494
ID   F19494 standard; DNA; 19 BP.
XX
AC   F19494;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human eosinophil peroxidase polynucleotide fragment #1061.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Claim 14; Page 145; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
```

```
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC   and antisense oligonucleotides used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 19 BP; 0 A; 8 C; 8 G; 3 T; 0 other;

  Query Match             100.0%;  Score 19;  DB 21;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 9.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           |||||||||||||||||||
Db       1 gcgctcggcctggtcccgg 19


RESULT   4
A33372
ID   A33372 standard; DNA; 19 BP.
XX
AC   A33372;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Low adenosine antisense oligonucleotide SEQ ID NO:1061.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Claim 18; Page 398; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. A32313 to A35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC   to A33992) are specifically claimed ONs from the present invention.
CC   N.B. Sequences given in the disclosure of the present invention do not
CC   match up with their corresponding SEQ ID NO: sequences given in the
CC   sequence listing.
XX
SQ   Sequence 19 BP; 0 A; 8 C; 8 G; 3 T; 0 other;

  Query Match             100.0%;  Score 19;  DB 21;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 9.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           |||||||||||||||||||
Db       1 gcgctcggcctggtcccgg 19


RESULT   5
T76132
ID   T76132 standard; DNA; 60 BP.
XX
AC   T76132;
XX
DT   12-SEP-1997  (first entry)
XX
DE   Human eosinophil peroxidase antisense oligonucleotide.
XX
KW   Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW   chronic obstructive pulmonary disease; bronchitis; ss.
XX
OS   Synthetic.
XX
PN   WO9640162-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US09306.
XX
PR   07-JUN-1995;   95US-0474497.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
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PI   Metzger WJ,  Nyce JW;
XX
DR   WPI; 1997-051871/05.
XX
PT   Treatment of airway diseases such as asthma - by topically applying
PT   adenosine-free antisense oligo:nucleotide to airway epithelium of
PT   subject
XX
PS   Claim 5; Page 27; 71pp; English.
XX
CC   A method for treating airway disease in a subject has been produced,
CC   which involves the topical administration of an essentially adenosine
CC   free antisense oligonucleotide (ON) to the airway epithelium of the
CC   subject. The present sequence is an antisense oligonucleotide specific
CC   for the human eosinophil peroxidase, targeted at the initiation
CC   codon. The method can be used to treat airway diseases such as cystic
CC   fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and
CC   other airway diseases characterised by an inflammatory response. By
CC   eliminating adenosine from the antisense ON, its liberation upon
CC   antisense degradation is prevented, thereby preventing adenosine-
CC   induced bronchoconstriction in patients with hyper-reactive airways.
XX
SQ   Sequence 60 BP; 0 A; 19 C; 22 G; 12 T; 7 other;


  Query Match             100.0%;  Score 19;  DB 18;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 8.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           ||||||||||||||||||||
Db      37 gcgctcggcctggtcccgg 55


RESULT   6
X53942
ID   X53942 standard; DNA; 60 BP.
XX
AC   X53942;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Intercellular adhesion molecule-1 (ICAM-1) antisense oligonucleotide.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 47; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (X52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences X55272-74. These multiple target
CC   oligonucleotides (specifically X55180-271) can be used for the antisense
CC   treatment of diseases and conditions. Typical diseases and conditions
CC   are those associated with impaired respiration and inflammation,
CC   including lung diseases, pulmonary vasoconstriction, inflammation,
CC   allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC   respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC   hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC   carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC   cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC   metastases, as well as all types of cancers which may metastasize or have
CC   metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 60 BP; 0 A; 19 C; 22 G; 12 T; 7 other;


  Query Match             100.0%;  Score 19;  DB 20;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 8.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           ||||||||||||||||||||
Db      37 gcgctcggcctggtcccgg 55


RESULT   7
F19504
ID   F19504 standard; DNA; 60 BP.
XX
AC   F19504;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human eosinophil peroxidase polynucleotide fragment #1071.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
```

```
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Claim 14; Page 145; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies).
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC   and antisense oligonucleotides used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 60 BP; 0 A; 19 C; 22 G; 12 T; 7 other;


  Query Match             100.0%;  Score 19;  DB 21;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 8.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           |||||||||||||||||||
Db      37 gcgctcggcctggtcccgg 55


RESULT   8
A33382
ID   A33382 standard; DNA; 60 BP.
XX
AC   A33382;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Low adenosine antisense oligonucleotide SEQ ID NO:1071.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Claim 18; Page 399; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. A32313 to A35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC   to A33992) are specifically claimed ONs from the present invention.
CC   N.B. Sequences given in the disclosure of the present invention do not
CC   match up with their corresponding SEQ ID NO: sequences given in the
CC   sequence listing.
XX
SQ   Sequence 60 BP; 0 A; 19 C; 22 G; 12 T; 7 other;


  Query Match             100.0%;  Score 19;  DB 21;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 8.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           |||||||||||||||||||
Db      37 gcgctcggcctggtcccgg 55


RESULT   9
X54603
ID   X54603 standard; DNA; 272 BP.
XX
AC   X54603;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Eosinophil peroxidase antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
```

KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US19419.
XX
PR 09-JUN-1998; 98US-0093972.
PR 17-SEP-1997; 97US-0059160.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
XX
PS Disclosure; Page 46; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (X52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences X55272-74. These multiple target
CC oligonucleotides (specifically X55180-271) can be used for the antisense
CC treatment of diseases and conditions. Typical diseases and conditions
CC are those associated with impaired respiration and inflammation,
CC including lung diseases, pulmonary vasoconstriction, inflammation,
CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC metastases, as well as all types of cancers which may metastasize or have
CC metastasized to the lungs, including breast and prostate cancer.
XX
SQ Sequence 272 BP; 0 A; 85 C; 98 G; 82 T; 7 other;

Query Match 100.0%; Score 19; DB 20; Length 272;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGCTCGGCCTGGTCCCGG 19
||||||||||||||||||||
Db 1 gcgctcggcctggtcccgg 19

RESULT 10
F20172
ID F20172 standard; DNA; 272 BP.
XX
AC F20172;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide #1739.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Claim 14; Page 547; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 272 BP; 0 A; 85 C; 98 G; 82 T; 7 other;

Query Match 100.0%; Score 19; DB 21; Length 272;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGCTCGGCCTGGTCCCGG 19
||||||||||||||||||||
Db 1 gcgctcggcctggtcccgg 19

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RESULT  11
A34050
ID   A34050 standard; DNA; 272 BP.
XX
AC   A34050;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:1739.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Disclosure; Page 481; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. A32313 to A35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC   to A33992) are specifically claimed ONs from the present invention.
CC   N.B. Sequences given in the disclosure of the present invention do not
CC   match up with their corresponding SEQ ID NO: sequences given in the
CC   sequence listing.
XX
SQ   Sequence 272 BP; 0 A; 85 C; 98 G; 82 T; 7 other;

  Query Match           100.0%;  Score 19;  DB 21;  Length 272;
  Best Local Similarity  100.0%;  Pred. No. 7.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           |||||||||||||||||||
Db       1 gcgctcggcctggtcccgg 19


RESULT  12
Z45456/c
ID   Z45456 standard; DNA; 2272 BP.
XX
AC   Z45456;
XX
DT   06-APR-2000  (first entry)
XX
DE   Nucleotide sequence of the human eosinophil peroxidase (EPO).
XX
KW   Human; eosinophil peroxidase; EPO; blood; oxydo-reductase;
KW   respiratory system tissue; ss.
XX
OS   Homo sapiens.
XX
PN   FR2780412-A1.
XX
PD   31-DEC-1999.
XX
PF   30-JUN-1998;   98FR-0008280.
XX
PR   30-JUN-1998;   98FR-0008280.
XX
PA   (HELI-) HELIX BIOTECHNOLOGIES SARL.
XX
PI   Gautier C,  Duport JM;
XX
DR   WPI; 2000-118775/11.
XX
PT   New human recombinant eosinophil peroxidase, useful for replacing human
PT   eosinophil peroxidase -
XX
PS   Claim 3; Fig 1; 29pp; French.
XX
CC   The present sequence represents an expression cassette of a human
CC   eosinophil peroxidase (EPO). The sequence is derived from a
CC   BamHI-HindIII fragment. The specification describes the production of
CC   human EPO fragments by genetic engineering. The sequence was obtained
CC   from total RNA isolated from human blood. The EPO protein is from the
CC   family of oxydo-reductases. The molecular mass of the protein is
CC   about 71 kDa. The human EPO can be used in large scale industrial
CC   applications, especially for the research of new medicaments, e.g. the
CC   toxic effects of natural eosinophil peroxidase on the tissues of the
CC   respiratory system could be diminished or modulated by using a
CC   medicament directly acting on the EPO. Antibodies against the EPO
CC   protein can be used for immunodetection of the protein.
XX
SQ   Sequence 2272 BP; 461 A; 732 C; 627 G; 452 T; 0 other;

  Query Match           100.0%;  Score 19;  DB 21;  Length 2272;
  Best Local Similarity  100.0%;  Pred. No. 6.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           |||||||||||||||||||
Db     444 GCGCTCGGCCTGGTCCCGG 426


RESULT  13
F20923/c
ID   F20923 standard; DNA; 2558 BP.
XX
AC   F20923;
XX
DT   14-MAR-2001  (first entry)
```

XX
DE Human eosinophil peroxidase polynucleotide fragment #2490.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 144-145; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 2558 BP; 527 A; 820 C; 698 G; 513 T; 0 other;

Query Match 100.0%; Score 19; DB 21; Length 2558;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGCTCGGCCTGGTCCCGG 19
||||||||||||||||||||
Db 384 GCGCTCGGCCTGGTCCCGG 366

RESULT 14
A34801/c
ID A34801 standard; DNA; 2558 BP.
XX
AC A34801;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2490.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 647-648; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.

```
XX
SQ   Sequence 2558 BP; 527 A; 820 C; 698 G; 513 T; 0 other;


  Query Match             100.0%;  Score 19;  DB 21;  Length 2558;
  Best Local Similarity   100.0%;  Pred. No. 6.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db    384 GCGCTCGGCCTGGTCCCGG 366


RESULT  15
F21441
ID   F21441 standard; DNA; 6103 BP.
XX
AC   F21441;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human eosinophil peroxidase polynucleotide fragment #3008.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Disclosure; Page 142-143; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC   and antisense oligonucleotides used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 6103 BP; 1218 A; 1863 C; 1727 G; 1287 T; 8 other;


  Query Match             100.0%;  Score 19;  DB 21;  Length 6103;
  Best Local Similarity   100.0%;  Pred. No. 6.4;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db      1 gcgctcggcctggtcccgg 19


Search completed: April 20, 2001, 00:13:01
Job time: 10023 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:25:03 ; Search time 7150.85 Seconds
(without alignments)
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Title: US-09-016-464-20
Perfect score: 19
Sequence: 1 GCGCTCGGCCTGGTCCCGG 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	17.4	91.6	649	165	BE298972	BE298972 601119505
	3	16.4	86.3	293	131	BB360288	BB360288 BB360288
c	4	16.4	86.3	450	161	BE014616	BE014616 126415 MA
c	5	16.4	86.3	468	103	AI891550	AI891550 ul31e08.x
c	6	16.4	86.3	528	209	AQ650598	AQ650598 Sheared D
c	7	16.4	86.3	546	233	TA70F12Q	AL458174 T. brucei
c	8	16.4	86.3	547	145	BF189303	BF189303 234766 MA
	9	16.4	86.3	1086	138	BE730153	BE730153 601560672
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	12	16	84.2	860	146	BF278046	BF278046 GA__Eb003
	13	16	84.2	908	119	AW729536	AW729536 GA__Ea002
c	14	15.8	83.2	109	14	AA971455	AA971455 op81c03.s
c	15	15.8	83.2	127	168	BF721315	BF721315 mab65d09.
	16	15.8	83.2	154	143	BF058495	BF058495 7k31d11.x
	17	15.8	83.2	163	160	BB564618	BB564618 BB564618
c	18	15.8	83.2	195	22	AI602991	AI602991 UI-R-AC1-

	19	15.8	83.2	197	168	BF730625	BF730625 mab65d09.
	20	15.8	83.2	244	24	AI717676	AI717676 UI-R-Y0-a
c	21	15.8	83.2	245	24	AI713617	AI713617 UI-R-AG1-
	22	15.8	83.2	268	23	AI699091	AI699091 tx56b11.x
c	23	15.8	83.2	283	24	AI709707	AI709707 UI-R-AG1-
c	24	15.8	83.2	310	116	AW525396	AW525396 UI-R-BJ0p
c	25	15.8	83.2	314	110	AW045268	AW045268 UI-M-BH1-
c	26	15.8	83.2	338	115	AW445253	AW445253 81210 MAR
	27	15.8	83.2	351	158	W30194	W30194 mc26g08.r1
	28	15.8	83.2	358	147	BF396472	BF396472 UI-R-BS2-
	29	15.8	83.2	360	113	AW321852	AW321852 uo20b06.x
	30	15.8	83.2	362	231	CNS03XVU	AL265539 Tetraodon
c	31	15.8	83.2	364	162	BE109821	BE109821 UI-R-BJ1-
	32	15.8	83.2	366	1	AA024123	AA024123 mi01c02.r
c	33	15.8	83.2	390	17	AI177468	AI177468 EST221098
	34	15.8	83.2	393	169	BF777094	BF777094 288912 MA
c	35	15.8	83.2	402	13	AA924731	AA924731 UI-R-A1-e
c	36	15.8	83.2	402	23	AI704042	AI704042 UI-R-AC1-
	37	15.8	83.2	406	19	AI325344	AI325344 mi01c02.y
	38	15.8	83.2	422	30	AV606734	AV606734 AV606734
	39	15.8	83.2	425	168	BF708484	BF708484 MI-P-AY0-
c	40	15.8	83.2	433	14	AA956707	AA956707 UI-R-E1-f
c	41	15.8	83.2	444	115	AW435374	AW435374 UI-R-BJ0p
c	42	15.8	83.2	455	24	AI712459	AI712459 UI-R-AF1-
c	43	15.8	83.2	457	24	AI710976	AI710976 UI-R-AE1-
c	44	15.8	83.2	463	162	BE100455	BE100455 UI-R-BJ1-
	45	15.8	83.2	464	17	AI226787	AI226787 uj15f10.y

ALIGNMENTS

RESULT 1
AI521798
LOCUS AI521798 493 bp mRNA EST 13-APR-1999
DEFINITION ti82e09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138536 3', mRNA sequence.
ACCESSION AI521798
VERSION AI521798.1 GI:4435933
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 493)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 903 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 464.
FEATURES Location/Qualifiers
source 1. .493
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2138536"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 75 a 168 c 175 g 74 t 1 others
ORIGIN

Query Match 91.6%; Score 17.4; DB 21; Length 493;
Best Local Similarity 94.7%; Pred. No. 5.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCGCTCGGCCTGGTCCCGG 19
||||||| |||||||||||
Db 387 GCGCTCGCCCTGGTCCCGG 405

RESULT 2
BE298972
LOCUS BE298972 649 bp mRNA EST 20-JUL-2000
DEFINITION 601119505F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029448 5', mRNA sequence.
ACCESSION BE298972
VERSION BE298972.1 GI:9182719
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 649)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM89 row: i column: 01
High quality sequence stop: 449.
FEATURES Location/Qualifiers
source 1. .649
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3029448"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 124 a 241 c 169 g 115 t
ORIGIN

Query Match 91.6%; Score 17.4; DB 165; Length 649;
Best Local Similarity 94.7%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCGCTCGGCCTGGTCCCGG 19
||||||||||||| |||||

```
Db    496 GCGCTCGGCCTGGCCCCGG 514


RESULT   3
BB360288
LOCUS       BB360288      293 bp    mRNA            EST       12-JUL-2000
DEFINITION  BB360288 RIKEN full-length enriched, adult male corpus striatum Mus
            musculus cDNA clone C030046E07 3' similar to AF039218 Rattus
            norvegicus postsynaptic density protein (citron) mRNA, mRNA
            sequence.
ACCESSION   BB360288
VERSION     BB360288.1  GI:9072116
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 293)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome-res@rtc.riken.go.jp,
            URL:http://genome.rtc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .293
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="C030046E07"
                     /clone_lib="RIKEN full-length enriched, adult male corpus
                     striatum"
                     /sex="male"
                     /tissue_type="corpus striatum"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 185.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI"
BASE COUNT       71 a     84 c     65 g     73 t
ORIGIN


  Query Match           86.3%;  Score 16.4;  DB 131;  Length 293;
  Best Local Similarity   94.4%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CGCTCGGCCTGGTCCCGG 19
           | ||||||||||||||||
Db     184 CTCTCGGCCTGGTCCCGG 201


RESULT   4
BE014616/c
LOCUS       BE014616      450 bp    mRNA            EST       09-JUL-2000
DEFINITION  126415 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BE014616
VERSION     BE014616.1  GI:8275635
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 55  row: H  column: 20
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .450
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 1PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
BASE COUNT       85 a    143 c    145 g     77 t
ORIGIN
```

```
  Query Match             86.3%;  Score 16.4;  DB 161;  Length 450;
  Best Local Similarity   94.4%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CGCTCGGCCTGGTCCCGG 19
          ||||||||| ||||||||
Db    380 CGCTCGGCCAGGTCCCGG 363


RESULT   5
AI891550/c
LOCUS       AI891550      468 bp    mRNA            EST       27-JUL-1999
DEFINITION  ul31e08.x1 Sugano mouse kidney mkia Mus musculus cDNA clone
            IMAGE:2099942 3', mRNA sequence.
ACCESSION   AI891550
VERSION     AI891550.1  GI:5597452
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 468)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: ul31e08.y1
            Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:996874
            Seq primer: custom primer used.
FEATURES             Location/Qualifiers
     source          1. .468
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:2099942"
                     /clone_lib="Sugano mouse kidney mkia"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
                     (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                     and cloned into distinct DraIII sites of the pME18S-FL3
                     vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                     be used to isolate the cDNA insert.  Size selection was
                     performed to exclude fragments <1.5kb.  Library
                     constructed by Dr. Sumio Sugano (University of Tokyo
                     Institute of Medical Science).  Custom primers for
                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                     primer CGACCTGCAGCTCGAGCACA."
BASE COUNT      107 a    113 c    127 g    121 t
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 103;  Length 468;
  Best Local Similarity   94.4%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CGCTCGGCCTGGTCCCGG 19
          | ||||||||||||||||
Db    110 CTCTCGGCCTGGTCCCGG 93


RESULT   6
AQ650598/c
LOCUS       AQ650598      528 bp    DNA             GSS       22-JUN-1999
DEFINITION  Sheared DNA-16O11.TR Sheared DNA Trypanosoma brucei genomic clone
            Sheared DNA-16O11, DNA sequence.
ACCESSION   AQ650598
VERSION     AQ650598.1  GI:5143784
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
            Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.
            , Fraser,C. and Adams,M.
  TITLE     Determination of clone end sequences from Trypanosoma brucei GUTat
            10.1 sheared DNA library
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: Sheared DNA-16O11.TF
            Contact: Najib M. El-Sayed
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: nelsayed@tigr.org
            Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
            DNA library constructed at TIGR. Clones will be available for
            distribution through ATCC. Sheared DNA end sequences search page:
            http://www.tigr.org/tdb/mdb/tbdb/.
            Seq primer: M13-Reverse
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .528
                     /organism="Trypanosoma brucei"
                     /strain="TREU927/4 GUTat 10.1"
                     /db_xref="taxon:5691"
                     /clone="Sheared DNA-16O11"
                     /clone_lib="Sheared DNA"
                     /note="Vector: pUC18; Site_1: SmaI; Constructed at The
                     Institute for Genomic Research (TIGR), Rockville, MD.
                     Genomic DNA isolated from a cloned population of
                     Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
                     sheared to give a tight size distribution (approx 2 kb).
                     The v + i method used for the library construction is
                     described in detail in Smith, H.O. and Venter, J.C.
                     (Making small insert libraries for whole genome shotgun
                     sequencing projects.  In Genome Sequencing: A Practical
                     Approach, eds. M. Vaudin and B. Barell, Oxford University
                     Press, 1999)."
BASE COUNT      162 a    122 c    128 g    116 t
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 209;  Length 528;
  Best Local Similarity   94.4%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCG 18
          |||||| ||||||||||||
Db    266 GCGCTCAGCCTGGTCCCG 249


RESULT   7
TA70F12Q/c
LOCUS       TA70F12Q      546 bp    DNA             GSS       13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 70f12, reverse sequence,
            genomic survey sequence.
ACCESSION   AL458174
```

```
VERSION     AL458174.1  GI:11859936
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 546)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .546
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="70f12"
BASE COUNT      152 a    149 c    134 g    111 t
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 233;  Length 546;
  Best Local Similarity   94.4%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCG 18
          |||||| ||||||||||
Db    460 GCGCTCAGCCTGGTCCCG 443


RESULT   8
BF189303/c
LOCUS       BF189303      547 bp    mRNA            EST       02-NOV-2000
DEFINITION  234766 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BF189303
VERSION     BF189303.1  GI:11072672
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 547)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 57  row: B  column: 1
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .547
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 2PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT       90 a    176 c    174 g    107 t
ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 145;  Length 547;
  Best Local Similarity   94.4%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CGCTCGGCCTGGTCCCGG 19
          |||||||||| ||||||||
Db    145 CGCTCGGCCAGGTCCCGG 128


RESULT   9
BE730153
LOCUS       BE730153     1086 bp    mRNA            EST       15-SEP-2000
DEFINITION  601560672F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3830632 5',
            mRNA sequence.
ACCESSION   BE730153
VERSION     BE730153.1  GI:10144145
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1086)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM504  row: o  column: 17
            High quality sequence start: 125
            High quality sequence stop: 593.
FEATURES             Location/Qualifiers
     source          1. .1086
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3830632"
                     /clone_lib="NIH_MGC_20"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      147 a    403 c    351 g    185 t
```

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ORIGIN


  Query Match             86.3%;  Score 16.4;  DB 138;  Length 1086;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCG 18
          |||| ||||||||||||||
Db    609 GCGCGCGGCCTGGTCCCG 626


RESULT  10
BF268451
LOCUS       BF268451      490 bp    mRNA            EST       17-NOV-2000
DEFINITION  GA__Eb0001N06f Gossypium arboreum 7-10 dpa fiber library Gossypium
            arboreum cDNA clone GA__Eb0001N06f, mRNA sequence.
ACCESSION   BF268451
VERSION     BF268451.1  GI:11199446
KEYWORDS    EST.
SOURCE      Gossypium arboreum.
  ORGANISM  Gossypium arboreum
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
            Malvales; Malvaceae; Gossypium.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
            ,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
  TITLE     An integrated analysis of the genetics, development, and evolution
            of the cotton fiber
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            High quality sequence start: 23
            High quality sequence stop: 466.
FEATURES             Location/Qualifiers
     source          1. .490
                     /organism="Gossypium arboreum"
                     /strain="AKA"
                     /cultivar="8400"
                     /db_xref="taxon:29729"
                     /clone="GA__Eb0001N06f"
                     /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
                     /tissue_type="Fibers isolated from bolls harvested 7-10
                     dpa"
                     /lab_host="E. coli"
                     /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT       90 a    196 c     77 g    126 t      1 others
ORIGIN


  Query Match             84.2%;  Score 16;  DB 146;  Length 490;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCTCGGCCTGGTCCCG 18
          ||||||||||||||||
Db    440 GCTCGGCCTGGTCCCG 455


RESULT  11
BE741923/c
LOCUS       BE741923      810 bp    mRNA            EST       15-SEP-2000
DEFINITION  601593721F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947620 5',
            mRNA sequence.
ACCESSION   BE741923
VERSION     BE741923.1  GI:10155915
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 810)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM809  row: j  column: 05
            High quality sequence start: 11
            High quality sequence stop: 655.
FEATURES             Location/Qualifiers
     source          1. .810
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3947620"
                     /clone_lib="NIH_MGC_9"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      153 a    291 c    218 g    148 t
ORIGIN


  Query Match             84.2%;  Score 16;  DB 139;  Length 810;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 CTCGGCCTGGTCCCGG 19
          ||||||||||||||||
Db     82 CTCGGCCTGGTCCCGG 67


RESULT  12
BF278046
LOCUS       BF278046      860 bp    mRNA            EST       17-NOV-2000
DEFINITION  GA__Eb0037L15f Gossypium arboreum 7-10 dpa fiber library Gossypium
            arboreum cDNA clone GA__Eb0037L15f, mRNA sequence.
ACCESSION   BF278046
VERSION     BF278046.1  GI:11209032
KEYWORDS    EST.
SOURCE      Gossypium arboreum.
  ORGANISM  Gossypium arboreum
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
            Malvales; Malvaceae; Gossypium.
REFERENCE   1  (bases 1 to 860)
  AUTHORS   Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
            ,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
  TITLE     An integrated analysis of the genetics, development, and evolution
            of the cotton fiber
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
```

```
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            High quality sequence start: 8
            High quality sequence stop: 729.
FEATURES              Location/Qualifiers
     source           1. .860
                      /organism="Gossypium arboreum"
                      /strain="AKA"
                      /cultivar="8400"
                      /db_xref="taxon:29729"
                      /clone="GA__Eb0037L15f"
                      /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
                      /tissue_type="Fibers isolated from bolls harvested 7-10
                      dpa"
                      /lab_host="E. coli"
                      /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT      193 a    278 c    159 g    229 t      1 others
ORIGIN


  Query Match             84.2%;  Score 16;  DB 146;  Length 860;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCTCGGCCTGGTCCCG 18
          ||||||||||||||||
Db    439 GCTCGGCCTGGTCCCG 454


RESULT  13
AW729536
LOCUS       AW729536      908 bp    mRNA            EST       16-NOV-2000
DEFINITION  GA__Ea0025E24 Gossypium arboreum 7-10 dpa fiber library Gossypium
            arboreum cDNA clone GA__Ea0025E24, mRNA sequence.
ACCESSION   AW729536
VERSION     AW729536.1  GI:7627132
KEYWORDS    EST.
SOURCE      Gossypium arboreum.
  ORGANISM  Gossypium arboreum
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
            Malvales; Malvaceae; Gossypium.
REFERENCE   1  (bases 1 to 908)
  AUTHORS   Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
            ,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
  TITLE     An integrated analysis of the genetics, development, and evolution
            of the cotton fiber
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            High quality sequence stop: 908.
FEATURES              Location/Qualifiers
     source           1. .908
                      /organism="Gossypium arboreum"
                      /strain="AKA"
                      /cultivar="8400"
                      /db_xref="taxon:29729"
                      /clone="GA__Ea0025E24"
                      /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
                      /tissue_type="Fibers isolated from bolls harvested 7-10
                      dpa"
                      /lab_host="E. coli"
                      /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT      204 a    285 c    174 g    244 t      1 others
ORIGIN


  Query Match             84.2%;  Score 16;  DB 119;  Length 908;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCTCGGCCTGGTCCCG 18
          ||||||||||||||||
Db    447 GCTCGGCCTGGTCCCG 462


RESULT  14
AA971455/c
LOCUS       AA971455      109 bp    mRNA            EST       07-JUL-1998
DEFINITION  op81c03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1583236 3' similar to gb:X52560_cds1 CCAAT/ENHANCER BINDING
            PROTEIN BETA (HUMAN);, mRNA sequence.
ACCESSION   AA971455
VERSION     AA971455.1  GI:3146745
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 109)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 2107   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .109
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1583236"
                      /clone_lib="Soares_NFL_T_GBC_S1"
                      /lab_host="DH10B"
                      /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                      a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                      Equal amounts of plasmid DNA from three normalized
                      libraries (fetal lung NbHL19W, testis NHT, and B-cell
                      NCI_CGAP_GCB1) were mixed, and ss circles were made in
                      vitro. Following HAP purification, this DNA was used as
                      tracer in a subtractive hybridization reaction. The driver
                      was PCR-amplified cDNAs from pools of 5,000 clones made
                      from the same 3 libraries. The pools consisted of
                      I.M.A.G.E. clones 297480-302087, 682632-687239,
                      726408-728711, and 729096-731399. Subtraction by Bento
                      Soares and M. Fatima Bonaldo.  "
BASE COUNT       29 a     27 c     42 g     11 t
ORIGIN


  Query Match             83.2%;  Score 15.8;  DB 14;  Length 109;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||| ||| |||
Db     51 GCGCTCGGCCTTGTCGCGG 33


RESULT  15
BF721315/c
LOCUS       BF721315      127 bp    mRNA            EST       03-JAN-2001
DEFINITION  mab65d09.y1 Soares_thymus_2NbMT Mus musculus cDNA clone
```

```
            IMAGE:3975209 5', mRNA sequence.
ACCESSION   BF721315
VERSION     BF721315.1  GI:12022317
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 127)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1475241
            Seq primer: -40RP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .127
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3975209"
                     /clone_lib="Soares_thymus_2NbMT"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT       20 a     49 c     48 g     10 t
ORIGIN


  Query Match             83.2%;  Score 15.8;  DB 168;  Length 127;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           |||| |||||||| |||||
Db      41 GCGCGCGGCCTGGGCCCGG 23


Search completed: April 19, 2001, 23:25:06
Job time: 8183 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:03:47 ; Search time 280.46 Seconds
(without alignments)
11.829 Million cell updates/sec

Title: US-09-016-464-20
Perfect score: 19
Sequence: 1 GCGCTCGGCCTGGTCCCGG 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15.8	83.2	1185	2	US-08-628-039-9	Sequence 9, Appli
	2	15.8	83.2	1185	3	US-08-912-205-9	Sequence 9, Appli
	3	15.8	83.2	1401	1	US-07-843-949A-3	Sequence 3, Appli
	4	15.8	83.2	1401	2	US-08-218-978-3	Sequence 3, Appli
	5	15.8	83.2	9960	3	US-08-822-586-46	Sequence 46, Appl
	6	15.8	83.2	20235	1	US-07-642-734C-3	Sequence 3, Appli
	7	15.8	83.2	20235	3	US-08-439-009A-3	Sequence 3, Appli
	8	15.8	83.2	35081	2	US-08-752-760A-1	Sequence 1, Appli
	9	15.4	81.1	3293	2	US-08-442-809A-75	Sequence 75, Appl
	10	14.8	77.9	24	3	US-08-840-316-93	Sequence 93, Appl
	11	14.8	77.9	24	4	US-08-809-523-93	Sequence 93, Appl
	12	14.8	77.9	24	5	PCT-US93-08849A-93	Sequence 93, Appl
	13	14.8	77.9	24	5	PCT-US93-08849-93	Sequence 93, Appl
c	14	14.8	77.9	99	1	US-08-240-049B-9	Sequence 9, Appli
c	15	14.8	77.9	99	5	PCT-US95-13703-11	Sequence 11, Appl
c	16	14.8	77.9	102	1	US-08-259-148A-11	Sequence 11, Appl
c	17	14.8	77.9	102	1	US-08-484-054-11	Sequence 11, Appl
c	18	14.8	77.9	102	2	US-07-876-941A-11	Sequence 11, Appl
c	19	14.8	77.9	372	1	US-08-240-049B-3	Sequence 3, Appli
c	20	14.8	77.9	372	5	PCT-US95-13703-9	Sequence 9, Appli
c	21	14.8	77.9	1457	4	US-09-444-053-3	Sequence 3, Appli
c	22	14.8	77.9	1554	1	US-08-469-486-1	Sequence 1, Appli
c	23	14.8	77.9	1554	2	US-08-469-658-1	Sequence 1, Appli
c	24	14.8	77.9	1983	1	US-08-240-049B-1	Sequence 1, Appli
c	25	14.8	77.9	2049	1	US-08-259-148A-3	Sequence 3, Appli
c	26	14.8	77.9	2049	1	US-08-484-054-3	Sequence 3, Appli
c	27	14.8	77.9	2049	2	US-07-876-941A-3	Sequence 3, Appli
c	28	14.8	77.9	2049	5	PCT-US95-13703-1	Sequence 1, Appli
c	29	14.8	77.9	2094	1	US-08-259-148A-1	Sequence 1, Appli
c	30	14.8	77.9	2094	1	US-08-484-054-1	Sequence 1, Appli
c	31	14.8	77.9	2094	2	US-07-876-941A-1	Sequence 1, Appli
c	32	14.8	77.9	7168	3	US-08-840-316-4	Sequence 4, Appli
c	33	14.8	77.9	7168	4	US-08-809-523-4	Sequence 4, Appli
c	34	14.8	77.9	7168	5	PCT-US93-08849A-4	Sequence 4, Appli
c	35	14.8	77.9	7168	5	PCT-US93-08849-4	Sequence 4, Appli
c	36	14.8	77.9	7195	4	US-08-478-507-6	Sequence 6, Appli
c	37	14.8	77.9	14636	4	US-09-173-914-6	Sequence 6, Appli
c	38	14.8	77.9	30001	1	US-08-125-468-1	Sequence 1, Appli
c	39	14.8	77.9	30001	2	US-08-474-933-1	Sequence 1, Appli
c	40	14.4	75.8	525	3	US-08-911-853-18	Sequence 18, Appl
	41	14.4	75.8	1288	2	US-08-743-637B-171	Sequence 171, App
	42	14.4	75.8	1288	3	US-08-526-840B-171	Sequence 171, App
	43	14.4	75.8	7171	4	US-08-478-507-10	Sequence 10, Appl
c	44	14.4	75.8	7210	2	US-08-257-963B-10	Sequence 10, Appl
c	45	14.4	75.8	7210	5	PCT-US95-07201-10	Sequence 10, Appl

ALIGNMENTS

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RESULT   1
US-08-628-039-9
; Sequence 9, Application US/08628039
; Patent No. 5942660
;  GENERAL INFORMATION:
;    APPLICANT:  Gruys, Kenneth J.
;    APPLICANT:  Mitsky, Timothy A.
;    APPLICANT:  Kishore, Ganesh M.
;    APPLICANT:  Slater, Steven C.
;    APPLICANT:  Padgette, Stephen R.
;    APPLICANT:  Stark, David M.
;    APPLICANT:  Hinchee, Maud A. W.
;    APPLICANT:  Clemente, Thomas E.
;    APPLICANT:  Connor-Ward, Dannette V.
;    APPLICANT:  Fedele, Mary J.
;    APPLICANT:  Fry, Joyce E.
;    APPLICANT:  Howe, Arlene R.
;    APPLICANT:  Rozman, Renee J.
;    TITLE OF INVENTION:  Methods of Optimizing Substrate Pools and
;    TITLE OF INVENTION:  Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval
;    TITLE OF INVENTION:  in Bacteria and Plants
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gary M. Bond, Monsanto Company, A3SB
;      STREET:  800 No. 5942660th Lindbergh Boulevard
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63167
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/628,039
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:  13-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bond, Gary
;      REGISTRATION NUMBER:  29,283
;      REFERENCE/DOCKET NUMBER:  38-21(13585)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)694-3412
;      TELEFAX:  (314)695-5435
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  1185 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-628-039-9


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  Best Local Similarity   89.5%;  Pred. No. 74;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db    991 GCGCTCGGTCTGGACCCGG 1009


RESULT   2
US-08-912-205-9
; Sequence 9, Application US/08912205
; Patent No. 6091002
;  GENERAL INFORMATION:
;    APPLICANT:  Asrar, Jawed
;    APPLICANT:  Mitsky, Timothy A.
;    APPLICANT:  Shah, Devang T.
;    TITLE OF INVENTION:  Polyhydroxyalkanoates of narrow molecular
;    TITLE OF INVENTION:  weight distribution prepared in transgenic plants
;    NUMBER OF SEQUENCES:  11
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/912,205
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/673,388
;      FILING DATE:  28-JUN-1996
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1185 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-912-205-9


  Query Match             83.2%;  Score 15.8;  DB 3;  Length 1185;
  Best Local Similarity   89.5%;  Pred. No. 74;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db    991 GCGCTCGGTCTGGACCCGG 1009


RESULT   3
US-07-843-949A-3
; Sequence 3, Application US/07843949A
; Patent No. 5340935
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Paul J.
;    APPLICANT:  Streuli, Michel
;    APPLICANT:  Schlossman, Stuart F.
;    TITLE OF INVENTION:  DNAS ENCODING PROTEINS ACTIVE IN
;    TITLE OF INVENTION:  LYMPHOCYTE-MEDIATED CYTOTOXICITY
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;      SOFTWARE:  WordPerfect (Version 5.0)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/843,949A
;      FILING DATE:  19920219
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/460,678
;      FILING DATE:  January 5, 1990
;      APPLICATION NUMBER:  07/726,607
;      FILING DATE:  July 10, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  00530/021003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1401
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-07-843-949A-3


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  Best Local Similarity   89.5%;  Pred. No. 73;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db      6 GCCCTCGGCCTTGTCCCGG 24


RESULT   4
US-08-218-978-3
; Sequence 3, Application US/08218978
; Patent No. 5837811
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Paul J.
;    APPLICANT:  Streuli, Michel
;    APPLICANT:  Schlossman, Stuart F.
;    TITLE OF INVENTION:  DNAS ENCODING PROTEINS ACTIVE IN
;    TITLE OF INVENTION:  LYMPHOCYTE-MEDIATED CYTOTOXICITY
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;      SOFTWARE:  WordPerfect (Version 5.0)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/218,978
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/843,949
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;      FILING DATE:  February 19, 1992
;      APPLICATION NUMBER:  07/460,678
;      FILING DATE:  January 5, 1990
;      APPLICATION NUMBER:  07/726,607
;      FILING DATE:  July 10, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  00530/021003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1401
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-218-978-3


  Query Match             83.2%;  Score 15.8;  DB 2;  Length 1401;
  Best Local Similarity   89.5%;  Pred. No. 73;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db      6 GCCCTCGGCCTTGTCCCGG 24


RESULT   5
US-08-822-586-46
; Sequence 46, Application US/08822586
; Patent No. 6015890
;  GENERAL INFORMATION:
;    APPLICANT:  WIILIAM R. JACOBS, JR., JAMES M. MUSSER AND
;    APPLICANT:  AMALIO TELENTI
;    TITLE OF INVENTION:  AN EMBCAB OPERON OF MYCOBACTERIA AND
;    TITLE OF INVENTION:  MUTANTS THEREOF
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMSTER, ROTHSTEIN & EBENSTEIN
;      STREET:  90 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH 1.44 Mb STORAGE
;      MEDIUM TYPE:  DISKETTE
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/822,586
;      FILING DATE:  MARCH 20, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ELIZABETH A. BOGOSIAN
;      REGISTRATION NUMBER:  39,911
;      REFERENCE/DOCKET NUMBER:  96700/437
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 697-5995
;      TELEFAX:  (212) 286-0854 or 286-0082
;      TELEX:  TWX 710-581-4766
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9960
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
US-08-822-586-46


  Query Match             83.2%;  Score 15.8;  DB 3;  Length 9960;
  Best Local Similarity   89.5%;  Pred. No. 62;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
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Db   2655 GCGCTCGGCGTGGTACCGG 2673


RESULT   6
US-07-642-734C-3
; Sequence 3, Application US/07642734C
; Patent No. 5824513
;  GENERAL INFORMATION:
;    APPLICANT:  Katz, L
;    APPLICANT:  Donadio, S
;    APPLICANT:  Mcalpine, J B
;    TITLE OF INVENTION:  Recombinant DNA Method for Producing
;    TITLE OF INVENTION:  Erythromycin Analogs
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Edward H. Gorman
;      STREET:  Abbott Laboratories D377/AP6D-2 One Abbott
;      STREET:  Park Rd
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/642,734C
;      FILING DATE:  17-JAN-91
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Danckers, Andreas M
;      REGISTRATION NUMBER:  32652
;      REFERENCE/DOCKET NUMBER:  4952.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-937-9396
;      TELEFAX:  708-938-2623
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20235 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Saccharopolyspora erythraea
;      STRAIN:  NRRL 238
;    FEATURE:
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;      LOCATION:  19..10722
;      OTHER INFORMATION:  /codon_start= 19
;      OTHER INFORMATION:  /function= "gene eryA"
;      OTHER INFORMATION:  /product= "eryA ORF2 encoding modules 3 & 4 for
;      OTHER INFORMATION:  6-deoxyerythronolide B"
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;      LOCATION:  19..4470
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;      OTHER INFORMATION:  module 3"
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;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  beta-ketoacyl ACP synthase of module 3"
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;       NAME/KEY:  misc_feature
;       LOCATION:  1693..2670
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  acyltransferase domain module 3"
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;       NAME/KEY:  misc_feature
;       LOCATION:  3406..3921
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  beta-ketoreductase domain of module 3"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  4171..4428
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  acyl carrier domain of module 3"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  4471..10722
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  module 4"
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;       LOCATION:  4471..5847
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  beta-ketoacylACPsynhase domain of module"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  6054..7026
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  acyltransferase domain of module 4"
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;       LOCATION:  7165..9216
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  dehydratase and enoylreductase domains m"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  9433..9984
;       OTHER INFORMATION:  /function= "approximate span
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;       NAME/KEY:  misc_feature
;       LOCATION:  10225..10483
;       OTHER INFORMATION:  /function= "approximate span of
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;       NAME/KEY:  CDS
;       LOCATION:  10723..20235
;       OTHER INFORMATION:  /codon_start= 10723
;       OTHER INFORMATION:  /function= "gene =eryA"
;       OTHER INFORMATION:  /product= "orf3 encoding modules 5 & 6
;       OTHER INFORMATION:  6-deoxyerythronolide B formatio"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  10723..15165
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  module 5"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  10831..12174
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  beta-ketoacylACPsynthase domain of modul"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  12379..13350
;       OTHER INFORMATION:  /function= "approximatr span of
;       OTHER INFORMATION:  acyltransferase domain of module 5"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  14062..14610
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  beta-ketoreductase of module 5"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  14857..15114
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  acyl carrier domain of module 5"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  15166..20235
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  module 6"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  15172..16569
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  beta-ketoacylACPsynthase domain of modul"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  16768..17721
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  acyltransferase domain of module 6"
;     FEATURE:
;       NAME/KEY:  misc_feature
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;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  beta-ketoreductase domain of module 6"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  19149..19398
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;       OTHER INFORMATION:  acyl carrier domain of module 6"
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;       NAME/KEY:  misc_feature
;       LOCATION:  19492..20235
;       OTHER INFORMATION:  /function= "approximate span of
;       OTHER INFORMATION:  thioesterase domain of module 6"
US-07-642-734C-3


  Query Match             83.2%;  Score 15.8;  DB 1;  Length 20235;
  Best Local Similarity   89.5%;  Pred. No. 58;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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RESULT   7
US-08-439-009A-3
; Sequence 3, Application US/08439009A
; Patent No. 6004787
;  GENERAL INFORMATION:
;    APPLICANT:  Donadio, S
;    APPLICANT:  Katz, L
;    APPLICANT:  Mcalpine, J B
;    TITLE OF INVENTION:  Method of Directing Biosynthesis of
;    TITLE OF INVENTION:  Specific Polyketides
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Steven F. Weinstock
;      STREET:  Abbott Laboratories D377/AP6D-2 One Abbott
;      STREET:  Park Rd
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/439,009A
;      FILING DATE:  11-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Casuto, Dianne
;      REGISTRATION NUMBER:  40,943
;      REFERENCE/DOCKET NUMBER:  4952.US.D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  847-938-3137
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20235 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Saccharopolyspora erythraea
;      STRAIN:  NRRL 238
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..10722
;      OTHER INFORMATION:  /codon_start= 19
;      OTHER INFORMATION:  /function= "gene eryA"
;      OTHER INFORMATION:  /product= "eryA ORF2 encoding modules 3 & 4 for
;      OTHER INFORMATION:  6-deoxyerythronolide B"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  19..4470
;      OTHER INFORMATION:  /function= "approximate span of
;      OTHER INFORMATION:  module 3"
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;      NAME/KEY:  misc_feature
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;      OTHER INFORMATION:  acyltransferase domain module 3"
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;      LOCATION:  3406..3921
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;      OTHER INFORMATION:  module 4"
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;      OTHER INFORMATION:  /function= "gene =eryA"
;      OTHER INFORMATION:  /product= "orf3 encoding modules 5 & 6
;      OTHER INFORMATION:  6-deoxyerythronolide B formatio"
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;      NAME/KEY:  misc_feature
;      LOCATION:  10723..15165
;      OTHER INFORMATION:  /function= "approximate span of
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;      LOCATION:  12379..13350
;      OTHER INFORMATION:  /function= "approximatr span of
;      OTHER INFORMATION:  acyltransferase domain of module 5"
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;      NAME/KEY:  misc_feature
;      LOCATION:  14062..14610
;      OTHER INFORMATION:  /function= "approximate span of
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;      NAME/KEY:  misc_feature
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;      NAME/KEY:  misc_feature
;      LOCATION:  15166..20235
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;    FEATURE:
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;      LOCATION:  15172..16569
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;      NAME/KEY:  misc_feature
;      LOCATION:  16768..17721
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;      NAME/KEY:  misc_feature
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;      OTHER INFORMATION:  beta-ketoreductase domain of module 6"
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;      NAME/KEY:  misc_feature
;      LOCATION:  19149..19398
;      OTHER INFORMATION:  /function= "approximate span of
;      OTHER INFORMATION:  acyl carrier domain of module 6"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  19492..20235
;      OTHER INFORMATION:  /function= "approximate span of
;      OTHER INFORMATION:  thioesterase domain of module 6"
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US-08-439-009A-3


  Query Match             83.2%;  Score 15.8;  DB 3;  Length 20235;
  Best Local Similarity   89.5%;  Pred. No. 58;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
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Db  13732 GCGCTCGCCCTGGTCCAGG 13750


RESULT   8
US-08-752-760A-1
; Sequence 1, Application US/08752760A
; Patent No. 5877011
;  GENERAL INFORMATION:
;    APPLICANT:  Armentano, Donna
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Smith, Alan E.
;    TITLE OF INVENTION:  CHIMERIC ADENOVIRAL VECTORS
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Baker & Botts, L.L.P.
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/752,760A
;      FILING DATE:  20-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seide, Rochelle K
;      REGISTRATION NUMBER:  32,300
;      REFERENCE/DOCKET NUMBER:  A31385
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-705-5000
;      TELEFAX:  212-705-5020
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35081 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-752-760A-1


  Query Match             83.2%;  Score 15.8;  DB 2;  Length 35081;
  Best Local Similarity   89.5%;  Pred. No. 55;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
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Db   8391 GCGCTCGGGCAGGTCCCGG 8409


RESULT   9
US-08-442-809A-75
; Sequence 75, Application US/08442809A
; Patent No. 5976873
;  GENERAL INFORMATION:
;    APPLICANT:  Bohinski, Robert J.,
;    APPLICANT:  Whitsett, Jeffrey A.
;    TITLE OF INVENTION:  Nucleic Acid Sequences
;    TITLE OF INVENTION:  Controlling Lung Cell -
;    TITLE OF INVENTION:  Specific Gene Expression
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,809A
;      FILING DATE:  17-MAY-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,356
;      FILING DATE:  18-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  271010-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3293 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
;    FEATURE:
;      NAME/KEY:  human TTF-1 gene
US-08-442-809A-75


  Query Match             81.1%;  Score 15.4;  DB 2;  Length 3293;
  Best Local Similarity   94.1%;  Pred. No. 99;
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Qy      3 GCTCGGCCTGGTCCCGG 19
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Db   1631 GCTCGGCCTGGCCCCGG 1647


RESULT  10
US-08-840-316-93
; Sequence 93, Application US/08840316
; Patent No. 6054567
;  GENERAL INFORMATION:
;    APPLICANT:  Emerson, Suzanne U., Purcell, Robert H.,
;    APPLICANT:  Tsarev, Sergei. A., and Robinson, Robin A.
;    TITLE OF INVENTION:  Recombinant Proteins Of
;    TITLE OF INVENTION:  A Pakistani Strain Of Hepatitis E And Their
;    TITLE OF INVENTION:  Use In Diagnostic Methods And Vaccines
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
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;       COMPUTER:  IBM PC COMPATIBLE
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WORDPERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/840,316
;       FILING DATE:  11-APR-1997
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Richard W. Bork
;       REGISTRATION NUMBER:  36,459
;       REFERENCE/DOCKET NUMBER:  2026-4255
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 758-4800
;       TELEFAX:  (212) 751-6849
;   INFORMATION FOR SEQ ID NO:  93:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  24 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-840-316-93


  Query Match             77.9%;  Score 14.8;  DB 3;  Length 24;
  Best Local Similarity   88.9%;  Pred. No. 2.7e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCG 18
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Db       2 GCGCTGGGCCTGGTCACG 19


RESULT  11
US-08-809-523-93
; Sequence 93, Application US/08809523
; Patent No. 6207416
;  GENERAL INFORMATION:
;    APPLICANT:  Tsarev, Sergei. A., Emerson,
;    APPLICANT:  Suzanne U., Purcell, Robert H.
;    TITLE OF INVENTION:  Recombinant Proteins Of
;    TITLE OF INVENTION:  A Pakistani Strain Of Hepatitis E And Their
;    TITLE OF INVENTION:  Use In Diagnostic Methods And Vaccines
;    NUMBER OF SEQUENCES:  107
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN, L.L.P.
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/809,523
;      FILING DATE:  28-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13102
;      FILING DATE:  03-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US08/316,765
;      FILING DATE:  03-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/947,263
;      FILING DATE:  18-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Richard W. Bork
;      REGISTRATION NUMBER:  36,459
;      REFERENCE/DOCKET NUMBER:  2026-4032US4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  93:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-809-523-93


  Query Match             77.9%;  Score 14.8;  DB 4;  Length 24;
  Best Local Similarity   88.9%;  Pred. No. 2.7e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCG 18
           ||||| ||||||||| ||
Db       2 GCGCTGGGCCTGGTCACG 19


RESULT  12
PCT-US93-08849A-93
; Sequence 93, Application PC/TUS9308849A
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Recombinant Proteins Of
;    TITLE OF INVENTION:  A Pakistani Strain Of Hepatitis E And Their
;    TITLE OF INVENTION:  Use In Diagnostic Methods And Vaccines
;    NUMBER OF SEQUENCES:  98
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08849A
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US07/947,263
;      FILING DATE:  18-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  William S. Feiler
;      REGISTRATION NUMBER:  26,728
;      REFERENCE/DOCKET NUMBER:  2026-4032 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  93:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US93-08849A-93


  Query Match             77.9%;  Score 14.8;  DB 5;  Length 24;
  Best Local Similarity   88.9%;  Pred. No. 2.7e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCG 18
           ||||| ||||||||| ||
Db       2 GCGCTGGGCCTGGTCACG 19
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RESULT  13
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; Sequence 93, Application PC/TUS9308849
;  GENERAL INFORMATION:
;    APPLICANT:  Tsarev, Sergei A., Emerson,
;    APPLICANT:  Suzanne U., Purcell, Robert H.
;    TITLE OF INVENTION:  Recombinant Proteins Of
;    TITLE OF INVENTION:  A Pakistani Strain Of Hepatitis E And Their
;    TITLE OF INVENTION:  Use In Diagnostic Methods And Vaccines
;    NUMBER OF SEQUENCES:  98
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
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;      FILING DATE:  17-SEP-1993
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/947,263
;      FILING DATE:  18-SEP-1992
;      NAME:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bork, Richard, W.
;      REGISTRATION NUMBER:  36,459
;      REFERENCE/DOCKET NUMBER:  2026-4032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  93:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US93-08849-93


  Query Match             77.9%;  Score 14.8;  DB 5;  Length 24;
  Best Local Similarity   88.9%;  Pred. No. 2.7e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCG 18
           ||||| |||||||||| ||
Db       2 GCGCTGGGCCTGGTCACG 19


RESULT  14
US-08-240-049B-9/c
; Sequence 9, Application US/08240049B
; Patent No. 5686239
;  GENERAL INFORMATION:
;    APPLICANT:  Reyes, Gregory R.
;    APPLICANT:  Tam, Albert W.
;    APPLICANT:  Yarbough, Patrice O.
;    TITLE OF INVENTION:  Hepatitis E Virus Peptides and Methods
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/240,049B
;      FILING DATE:  09-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Charles K. Sholtz
;      REGISTRATION NUMBER:  38,615
;      REFERENCE/DOCKET NUMBER:  4600-0093.35; G32P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  99 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Hepatitis E Virus (Burma strain)
;      INDIVIDUAL ISOLATE:  406.4-2 region
US-08-240-049B-9


  Query Match             77.9%;  Score 14.8;  DB 1;  Length 99;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCG 18
           ||||| |||||||||| ||
Db      50 GCGCTGGGCCTGGTCACG 33


RESULT  15
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; Sequence 11, Application PC/TUS9513703
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;    APPLICANT:
;    TITLE OF INVENTION:  HEPATITIS E VIRUS ANTIGENS AND
;    TITLE OF INVENTION:  USES THEREFOR
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  P.O. Box 60850
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306-0850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13703
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0293.41
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  99 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Hepatitis E Virus (Burma strain)
;      INDIVIDUAL ISOLATE:  406.4-2 region
PCT-US95-13703-11


  Query Match             77.9%;  Score 14.8;  DB 5;  Length 99;
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  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCG 18
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Db      50 GCGCTGGGCCTGGTCACG 33


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GenCore version 4.5

OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-016-464-20
Perfect score: 19
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13168883 seqs, 2603265903 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	19	100.0	19	8	US-08-474-497-20	Sequence 20, Appl
	2	19	100.0	19	14	US-09-016-464-20	Sequence 20, Appl
	3	19	100.0	19	19	US-09-509-152A-1061	Sequence 1061, Ap
	4	19	100.0	60	19	US-09-509-152A-1071	Sequence 1071, Ap
	5	19	100.0	272	19	US-09-509-152A-1739	Sequence 1739, Ap
	6	19	100.0	367	18	US-09-496-911-3525	Sequence 3525, Ap
c	7	19	100.0	454	17	US-09-306-350A-2131	Sequence 2131, Ap
c	8	19	100.0	465	17	US-09-306-350A-1791	Sequence 1791, Ap
c	9	19	100.0	468	17	US-09-306-350A-2747	Sequence 2747, Ap
c	10	19	100.0	470	48	US-60-169-840-164	Sequence 164, App
c	11	19	100.0	520	24	US-09-637-888-5196	Sequence 5196, Ap
c	12	19	100.0	523	49	US-60-170-373-1322	Sequence 1322, Ap
c	13	19	100.0	2079	54	US-60-226-176-976	Sequence 976, App
c	14	19	100.0	2079	55	US-60-233-468-976	Sequence 976, App
c	15	19	100.0	2109	54	US-60-226-176-973	Sequence 973, App
c	16	19	100.0	2109	55	US-60-233-468-973	Sequence 973, App
c	17	19	100.0	2524	54	US-60-226-176-975	Sequence 975, App
c	18	19	100.0	2524	55	US-60-233-468-975	Sequence 975, App
c	19	19	100.0	2558	54	US-60-226-176-972	Sequence 972, App
c	20	19	100.0	2558	55	US-60-233-468-972	Sequence 972, App
c	21	19	100.0	2599	18	US-09-496-914A-5820	Sequence 5820, Ap
c	22	19	100.0	2718	25	US-09-652-121-6848	Sequence 6848, Ap
c	23	19	100.0	2718	25	US-09-652-124-9476	Sequence 9476, Ap
c	24	19	100.0	2718	25	US-09-652-814-9544	Sequence 9544, Ap
c	25	19	100.0	2718	29	US-09-736-119-1873	Sequence 1873, Ap
c	26	19	100.0	2732	49	US-60-172-373-15079	Sequence 15079, A
	27	19	100.0	7033	19	US-09-509-152A-2411	Sequence 2411, Ap
c	28	19	100.0	162083	54	US-60-226-176-974	Sequence 974, App
c	29	19	100.0	162083	55	US-60-233-468-974	Sequence 974, App
c	30	17.4	91.6	425	48	US-60-169-840-304	Sequence 304, App
c	31	17	89.5	237	17	US-09-304-517A-149744	Sequence 149744,
	32	17	89.5	963	25	US-09-652-124-8079	Sequence 8079, Ap
	33	17	89.5	963	25	US-09-652-911-8273	Sequence 8273, Ap
	34	16.4	86.3	250	25	US-09-654-617-380642	Sequence 380642,
	35	16.4	86.3	250	27	US-09-684-016-380642	Sequence 380642,
	36	16.4	86.3	533	52	US-60-209-830-3878	Sequence 3878, Ap
c	37	16.4	86.3	142530	53	US-60-212-664-303	Sequence 303, App
c	38	16	84.2	246	17	US-09-304-517A-148348	Sequence 148348,
c	39	16	84.2	246	25	US-09-654-617-48855	Sequence 48855, A
c	40	16	84.2	246	27	US-09-684-016-48855	Sequence 48855, A
c	41	16	84.2	246	29	US-09-733-089-10526	Sequence 10526, A
	42	16	84.2	350	52	US-60-207-458-85721	Sequence 85721, A
c	43	16	84.2	555	50	US-60-182-316-9259	Sequence 9259, Ap
	44	16	84.2	631	28	US-09-703-708-212	Sequence 212, App
	45	16	84.2	631	48	US-60-164-320-212	Sequence 212, App

ALIGNMENTS

```
RESULT   1
US-08-474-497-20
; Sequence 20, Application US/08474497
;  GENERAL INFORMATION:
;    APPLICANT:  Nyce, Jonathan W.
;    TITLE OF INVENTION:  Method of Treatment of Lung Diseases
;    TITLE OF INVENTION:  Using Antisense Oligonucleotides
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  Post Office Drawer 34009
;      CITY:  Charlotte
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,497
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5218-32
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 881-3140
;      TELEFAX:  (919) 881-3175
;      TELEX:  575102
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-474-497-20


  Query Match             100.0%;  Score 19;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db      1 GCGCTCGGCCTGGTCCCGG 19


RESULT   2
US-09-016-464-20
; Sequence 20, Application US/09016464
;   GENERAL INFORMATION:
;        APPLICANT: Nyce, Jonathan W.
;        TITLE OF INVENTION: Method of Treatment of Lung Diseases
;                            Using Antisense Oligonucleotides
;        NUMBER OF SEQUENCES: 44
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Kenneth D. Sibley
;             STREET: Post Office Drawer 34009
;             CITY: Charlotte
;             STATE: NC
;             COUNTRY: USA
;             ZIP: 28234
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/016,464
;             FILING DATE: 30-Jan-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/474,497
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sibley, Kenneth D.
;             REGISTRATION NUMBER: 31,665
;             REFERENCE/DOCKET NUMBER: 5218-32
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (919) 881-3140
;             TELEFAX: (919) 881-3175
;             TELEX: 575102
;   INFORMATION FOR SEQ ID NO: 20:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 19 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-016-464-20


  Query Match             100.0%;  Score 19;  DB 14;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db      1 GCGCTCGGCCTGGTCCCGG 19


RESULT   3
US-09-509-152A-1061
; Sequence 1061, Application US/09509152A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, JONATHAN W.
;        TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
;                            FORMULATIONS, KITS & APPLICATIONS
;        NUMBER OF SEQUENCES: 2419
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 CLARKE DRIVE
;             CITY: CRANBURY
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/509,152A
;             FILING DATE: 17-Mar-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/059,160
;             FILING DATE: 1997-09-17
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-00991
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1061:
;        SEQUENCE CHARACTERISTICS:
```

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;             LENGTH: 19 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1061:
US-09-509-152A-1061


  Query Match             100.0%;  Score 19;  DB 19;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db      1 GCGCTCGGCCTGGTCCCGG 19


RESULT   4
US-09-509-152A-1071
; Sequence 1071, Application US/09509152A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, JONATHAN W.
;        TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
;                            FORMULATIONS, KITS & APPLICATIONS
;        NUMBER OF SEQUENCES: 2419
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 CLARKE DRIVE
;             CITY: CRANBURY
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/509,152A
;             FILING DATE: 17-Mar-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/059,160
;             FILING DATE: 1997-09-17
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-00991
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1071:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 60 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: Genomic DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1071:
US-09-509-152A-1071


  Query Match             100.0%;  Score 19;  DB 19;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db     37 GCGCTCGGCCTGGTCCCGG 55


RESULT   5
US-09-509-152A-1739
; Sequence 1739, Application US/09509152A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, JONATHAN W.
;        TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
;                            FORMULATIONS, KITS & APPLICATIONS
;        NUMBER OF SEQUENCES: 2419
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 CLARKE DRIVE
;             CITY: CRANBURY
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/509,152A
;             FILING DATE: 17-Mar-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/059,160
;             FILING DATE: 1997-09-17
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-00991
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1739:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 272 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1739:
US-09-509-152A-1739


  Query Match             100.0%;  Score 19;  DB 19;  Length 272;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db      1 GCGCTCGGCCTGGTCCCGG 19


RESULT   6
US-09-496-911-3525
; Sequence 3525, Application US/09496911
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
;  TITLE OF INVENTION: From Various Libraries
;  FILE REFERENCE: 786
;  CURRENT APPLICATION NUMBER: US/09/496,911
;  CURRENT FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 13944
;  SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 3525
;   LENGTH: 367
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-496-911-3525


  Query Match             100.0%;  Score 19;  DB 18;  Length 367;
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  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db    227 gcgctcggcctggtcccgg 245


RESULT   7
US-09-306-350A-2131/c
; Sequence 2131, Application US/09306350A
; GENERAL INFORMATION:
;  APPLICANT:  Dickson, Mark C.
;  APPLICANT:  Drmanac, Radoje T.
;  APPLICANT:  Jones, Lee W.
;  APPLICANT:  Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  TITLE OF INVENTION:  Novel Nucleic Acid Sequences Obtained
;  TITLE OF INVENTION:  From Various cDNA Libraries
;  FILE REFERENCE:  20411-776
;  CURRENT APPLICATION NUMBER: US/09/306,350A
;  CURRENT FILING DATE:  1999-05-07
;  NUMBER OF SEQ ID NOS:  41304
;  SOFTWARE:  pt_CT_1 Version 1.1
; SEQ ID NO 2131
;   LENGTH: 454
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-306-350A-2131


  Query Match             100.0%;  Score 19;  DB 17;  Length 454;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db    163 GCGCTCGGCCTGGTCCCGG 145


RESULT   8
US-09-306-350A-1791/c
; Sequence 1791, Application US/09306350A
; GENERAL INFORMATION:
;  APPLICANT:  Dickson, Mark C.
;  APPLICANT:  Drmanac, Radoje T.
;  APPLICANT:  Jones, Lee W.
;  APPLICANT:  Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  TITLE OF INVENTION:  Novel Nucleic Acid Sequences Obtained
;  TITLE OF INVENTION:  From Various cDNA Libraries
;  FILE REFERENCE:  20411-776
;  CURRENT APPLICATION NUMBER: US/09/306,350A
;  CURRENT FILING DATE:  1999-05-07
;  NUMBER OF SEQ ID NOS:  41304
;  SOFTWARE:  pt_CT_1 Version 1.1
; SEQ ID NO 1791
;   LENGTH: 465
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(465)
;   OTHER INFORMATION: n = a,t,c or g
US-09-306-350A-1791


  Query Match             100.0%;  Score 19;  DB 17;  Length 465;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db    167 GCGCTCGGCCTGGTCCCGG 149


RESULT   9
US-09-306-350A-2747/c
; Sequence 2747, Application US/09306350A
; GENERAL INFORMATION:
;  APPLICANT:  Dickson, Mark C.
;  APPLICANT:  Drmanac, Radoje T.
;  APPLICANT:  Jones, Lee W.
;  APPLICANT:  Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  TITLE OF INVENTION:  Novel Nucleic Acid Sequences Obtained
;  TITLE OF INVENTION:  From Various cDNA Libraries
;  FILE REFERENCE:  20411-776
;  CURRENT APPLICATION NUMBER: US/09/306,350A
;  CURRENT FILING DATE:  1999-05-07
;  NUMBER OF SEQ ID NOS:  41304
;  SOFTWARE:  pt_CT_1 Version 1.1
; SEQ ID NO 2747
;   LENGTH: 468
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(468)
;   OTHER INFORMATION: n = a,t,c or g
US-09-306-350A-2747


  Query Match             100.0%;  Score 19;  DB 17;  Length 468;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db    409 GCGCTCGGCCTGGTCCCGG 391


RESULT  10
US-60-169-840-164/c
; Sequence 164, Application US/60169840
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
;  TITLE OF INVENTION: USES THEREOF
;  FILE REFERENCE: CL000164
;  CURRENT APPLICATION NUMBER: US/60/169,840
;  CURRENT FILING DATE: 1999-12-09
;  NUMBER OF SEQ ID NOS: 9628
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 164
;   LENGTH: 470
;   TYPE: DNA
;   ORGANISM: Human
US-60-169-840-164


  Query Match             100.0%;  Score 19;  DB 48;  Length 470;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db    369 GCGCTCGGCCTGGTCCCGG 351


RESULT  11
US-09-637-888-5196/c
; Sequence 5196, Application US/09637888
; GENERAL INFORMATION:
;  APPLICANT:  Curtis, Rory A. J.
```

```
;  APPLICANT:  Gearing, David P.
;  APPLICANT:  Kingsbury, Gillian A.
;  APPLICANT:  Holzman, Douglas A.
;  APPLICANT:  Weich, Nadine S.
;  APPLICANT:  Fraser, Christopher C.
;  APPLICANT:  Villeval, Jean-Luc M.G.
;  APPLICANT:  Goodearl, Andrew
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Pan, Yang
;  APPLICANT:  White, David
;  APPLICANT:  Hodge, Martin
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.1155-001
;  CURRENT APPLICATION NUMBER: US/09/637,888
;  CURRENT FILING DATE:  2000-08-06
;  PRIOR APPLICATION NUMBER:  60/147,937
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  10569
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 5196
;   LENGTH: 520
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(520)
;   OTHER INFORMATION: n = A,T,C or G
US-09-637-888-5196


  Query Match             100.0%;  Score 19;  DB 24;  Length 520;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db     69 GCGCTCGGCCTGGTCCCGG 51


RESULT  12
US-60-170-373-1322/c
; Sequence 1322, Application US/60170373
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTIENS AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL000149
;  CURRENT APPLICATION NUMBER: US/60/170,373
;  CURRENT FILING DATE: 1999-12-13
;  NUMBER OF SEQ ID NOS: 4282
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1322
;   LENGTH: 523
;   TYPE: DNA
;   ORGANISM: Human
US-60-170-373-1322


  Query Match             100.0%;  Score 19;  DB 49;  Length 523;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db    285 GCGCTCGGCCTGGTCCCGG 267


RESULT  13
US-60-226-176-976/c
; Sequence 976, Application US/60226176
; GENERAL INFORMATION:
;  APPLICANT:      Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  TITLE OF INVENTION:  Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE:  GX-0013-1 P
;  CURRENT APPLICATION NUMBER: US/60/226,176
;  CURRENT FILING DATE:  2000-08-16
;  NUMBER OF SEQ ID NOS:      2447
;  SOFTWARE:       PERL Program
; SEQ ID NO 976
;   LENGTH: 2079
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: EPX_cds.1
US-60-226-176-976


  Query Match             100.0%;  Score 19;  DB 54;  Length 2079;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db    351 GCGCTCGGCCTGGTCCCGG 333


RESULT  14
US-60-233-468-976/c
; Sequence 976, Application US/60233468
; GENERAL INFORMATION:
;  APPLICANT:      Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Valdes, Ana
;  TITLE OF INVENTION:  Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE:  GX-0013-2 P
;  CURRENT APPLICATION NUMBER: US/60/233,468
;  CURRENT FILING DATE:  2000-09-18
;  NUMBER OF SEQ ID NOS:      2488
;  SOFTWARE:       PERL Program
; SEQ ID NO 976
;   LENGTH: 2079
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: EPX_cds.1
US-60-233-468-976


  Query Match             100.0%;  Score 19;  DB 55;  Length 2079;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db    351 GCGCTCGGCCTGGTCCCGG 333


RESULT  15
US-60-226-176-973/c
; Sequence 973, Application US/60226176
; GENERAL INFORMATION:
;  APPLICANT:      Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  TITLE OF INVENTION:  Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE:  GX-0013-1 P
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;  CURRENT APPLICATION NUMBER: US/60/226,176
;  CURRENT FILING DATE:  2000-08-16
;  NUMBER OF SEQ ID NOS:      2447
;  SOFTWARE:       PERL Program
; SEQ ID NO 973
;   LENGTH: 2109
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GB:HSEP.1
US-60-226-176-973


  Query Match            100.0%;  Score 19;  DB 54;  Length 2109;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db    384 GCGCTCGGCCTGGTCCCGG 366


Search completed: April 20, 2001, 03:21:33
Job time: 14180 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:15:57 ; Search time 101.94 Seconds
(without alignments)
25.791 Million cell updates/sec

Title: US-09-016-464-20
Perfect score: 19
Sequence: 1 GCGCTCGGCCTGGTCCCGG 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 46985 seqs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	19	100.0	19	5	US-09-543-679A-1061	Sequence 1061, Ap
	2	19	100.0	60	5	US-09-543-679A-1071	Sequence 1071, Ap
	3	19	100.0	272	5	US-09-543-679A-1739	Sequence 1739, Ap
c	4	19	100.0	2558	5	US-09-543-679A-2490	Sequence 2490, Ap
	5	19	100.0	6103	5	US-09-543-679A-3008	Sequence 3008, Ap
c	6	19	100.0	6103	5	US-09-543-679A-3008	Sequence 3008, Ap
	7	19	100.0	7033	5	US-09-543-679A-2411	Sequence 2411, Ap
c	8	19	100.0	35459	5	US-09-543-679A-3003	Sequence 3003, Ap
	9	19	100.0	209274	5	US-09-543-679A-3004	Sequence 3004, Ap
	10	15.8	83.2	300	5	US-09-739-449-4003	Sequence 4003, Ap
c	11	15.8	83.2	2091	5	US-09-739-449-3607	Sequence 3607, Ap
	12	15.8	83.2	183820	5	US-09-739-449-209	Sequence 209, App
	13	15.4	81.1	974	5	US-09-819-308-9	Sequence 9, Appli
	14	15	78.9	15	5	US-09-543-679A-1740	Sequence 1740, Ap
	15	14.8	77.9	303	5	US-09-739-449-6709	Sequence 6709, Ap
	16	14.8	77.9	504	4	US-08-276-163D-9185	Sequence 9185, Ap
c	17	14.4	75.8	933	5	US-09-739-449-6367	Sequence 6367, Ap
c	18	14.4	75.8	1077	1	PCT-US01-10246-1	Sequence 1, Appli
c	19	14.4	75.8	24390	6	US-60-248-505-56	Sequence 56, Appl
c	20	14.4	75.8	24391	6	US-60-248-505-406	Sequence 406, App
	21	14.4	75.8	41100	6	US-60-248-822-5	Sequence 5, Appli
	22	14.2	74.7	490	4	US-08-276-163D-10820	Sequence 10820, A
	23	14.2	74.7	494	4	US-08-276-163D-7740	Sequence 7740, Ap
c	24	14.2	74.7	505	4	US-08-276-163D-14346	Sequence 14346, A
c	25	14.2	74.7	664	5	US-09-739-449-1933	Sequence 1933, Ap
	26	14.2	74.7	759	5	US-09-739-449-3332	Sequence 3332, Ap
	27	14.2	74.7	936	5	US-09-739-449-7872	Sequence 7872, Ap
	28	14.2	74.7	1254	5	US-09-739-449-2784	Sequence 2784, Ap
c	29	14.2	74.7	1534	6	US-60-248-505-1484	Sequence 1484, Ap
	30	14.2	74.7	1539	5	US-09-543-679A-2678	Sequence 2678, Ap
	31	14.2	74.7	1539	5	US-09-543-679A-2732	Sequence 2732, Ap
	32	14.2	74.7	1546	6	US-60-248-505-1741	Sequence 1741, Ap
	33	14.2	74.7	1956	5	US-09-739-449-7526	Sequence 7526, Ap
	34	14.2	74.7	2331	5	US-09-739-449-6958	Sequence 6958, Ap
	35	14.2	74.7	3055	6	US-60-248-505-1651	Sequence 1651, Ap
	36	14.2	74.7	3089	5	US-09-543-679A-2680	Sequence 2680, Ap
	37	14.2	74.7	4096	6	US-60-248-505-1910	Sequence 1910, Ap
c	38	14.2	74.7	5901	5	US-09-813-206-897	Sequence 897, App
c	39	14.2	74.7	9969	6	US-60-248-505-152	Sequence 152, App
c	40	14.2	74.7	9970	6	US-60-248-505-409	Sequence 409, App
c	41	14.2	74.7	16893	6	US-60-248-505-319	Sequence 319, App
c	42	14.2	74.7	27266	6	US-60-248-505-578	Sequence 578, App
	43	14.2	74.7	143551	5	US-09-739-449-203	Sequence 203, App
	44	14.2	74.7	160609	6	US-60-248-505-48	Sequence 48, Appl
	45	14.2	74.7	165200	5	US-09-739-449-205	Sequence 205, App

ALIGNMENTS

```
RESULT   1
US-09-543-679A-1061
; Sequence 1061, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1061:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 19 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1061:
US-09-543-679A-1061


  Query Match             100.0%;  Score 19;  DB 5;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db      1 GCGCTCGGCCTGGTCCCGG 19


RESULT   2
US-09-543-679A-1071
; Sequence 1071, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1071:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 60 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: Genomic DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1071:
US-09-543-679A-1071


  Query Match             100.0%;  Score 19;  DB 5;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db     37 GCGCTCGGCCTGGTCCCGG 55


RESULT   3
US-09-543-679A-1739
; Sequence 1739, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1739:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 272 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1739:
US-09-543-679A-1739


  Query Match             100.0%;  Score 19;  DB 5;  Length 272;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          ||||||||||||||||||||
Db      1 GCGCTCGGCCTGGTCCCGG 19


RESULT   4
US-09-543-679A-2490/c
; Sequence 2490, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
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;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2490:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2558 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2490:
US-09-543-679A-2490


  Query Match             100.0%;  Score 19;  DB 5;  Length 2558;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db    384 GCGCTCGGCCTGGTCCCGG 366


RESULT   5
US-09-543-679A-3008
; Sequence 3008, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION;
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;    INFORMATION FOR SEQ ID NO: 3008:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 6103base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 3008:
US-09-543-679A-3008


  Query Match             100.0%;  Score 19;  DB 5;  Length 6103;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db      1 GCGCTCGGCCTGGTCCCGG 19


RESULT   6
US-09-543-679A-3008/c
; Sequence 3008, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3008:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 6103base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3008:
US-09-543-679A-3008


  Query Match             100.0%;  Score 19;  DB 5;  Length 6103;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db   3929 GCGCTCGGCCTGGTCCCGG 3911


RESULT   7
US-09-543-679A-2411
; Sequence 2411, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
```

```
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2411:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 7033 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2411:
US-09-543-679A-2411


  Query Match            100.0%;  Score 19;  DB 5;  Length 7033;
  Best Local Similarity  100.0%;  Pred. No. 1.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db    238 GCGCTCGGCCTGGTCCCGG 256


RESULT   8
US-09-543-679A-3003/c
; Sequence 3003, Application US/09543679A
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3003:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 35459 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3003:
US-09-543-679A-3003


  Query Match            100.0%;  Score 19;  DB 5;  Length 35459;
  Best Local Similarity  100.0%;  Pred. No. 1;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCGG 19
          |||||||||||||||||||
Db  22481 GCGCTCGGCCTGGTCCCGG 22463


RESULT   9
US-09-543-679A-3004
; Sequence 3004, Application US/09543679A
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3004:
;       SEQUENCE CHARACTERISTICS:
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;             LENGTH: 209274 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3004:
US-09-543-679A-3004


  Query Match             100.0%;  Score 19;  DB 5;  Length 209274;
  Best Local Similarity   100.0%;  Pred. No. 0.77;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           ||||||||||||||||||||
Db     238 GCGCTCGGCCTGGTCCCGG 256


RESULT  10
US-09-739-449-4003
; Sequence 4003, Application US/09739449
; GENERAL INFORMATION:
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15490)C
;  CURRENT APPLICATION NUMBER: US/09/739,449
;  CURRENT FILING DATE:  2000-12-19
;  PRIOR APPLICATION NUMBER: US 09/514,000
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 4003
;   LENGTH: 300
;   TYPE: DNA
;   ORGANISM: Agrobacterium tumefaciens
US-09-739-449-4003


  Query Match             83.2%;  Score 15.8;  DB 5;  Length 300;
  Best Local Similarity   89.5%;  Pred. No. 47;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           |||||||||  ||||| |||
Db      79 gcgctcggcatggtctcgg 97


RESULT  11
US-09-739-449-3607/c
; Sequence 3607, Application US/09739449
; GENERAL INFORMATION:
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15490)C
;  CURRENT APPLICATION NUMBER: US/09/739,449
;  CURRENT FILING DATE:  2000-12-19
;  PRIOR APPLICATION NUMBER: US 09/514,000
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 3607
;   LENGTH: 2091
;   TYPE: DNA
;   ORGANISM: Agrobacterium tumefaciens
US-09-739-449-3607


  Query Match             83.2%;  Score 15.8;  DB 5;  Length 2091;
  Best Local Similarity   89.5%;  Pred. No. 35;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           |||  ||||||| ||||||
Db     975 GCGTTCGGCCTGCTCCCGG 957


RESULT  12
US-09-739-449-209
; Sequence 209, Application US/09739449
; GENERAL INFORMATION:
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15490)C
;  CURRENT APPLICATION NUMBER: US/09/739,449
;  CURRENT FILING DATE:  2000-12-19
;  PRIOR APPLICATION NUMBER: US 09/514,000
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 209
;   LENGTH: 183820
;   TYPE: DNA
;   ORGANISM: Agrobacterium tumefaciens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(183820)
;   OTHER INFORMATION: unsure at all n locations
US-09-739-449-209


  Query Match             83.2%;  Score 15.8;  DB 5;  Length 183820;
  Best Local Similarity   89.5%;  Pred. No. 18;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCCGG 19
           |||  |||||||| ||||||
Db   23951 gcgttcggcctgctcccgg 23969


RESULT  13
US-09-819-308-9
; Sequence 9, Application US/09819308
; GENERAL INFORMATION:
;  APPLICANT: Noteborn, Mathieu
;  APPLICANT:  Danen-van Oorschot, Astrid
;  APPLICANT:  Rohn, Jennifer
;  TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
;  FILE REFERENCE: 2906-4820US
;  CURRENT APPLICATION NUMBER: US/09/819,308
;  CURRENT FILING DATE:  2001-03-27
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 974
;   TYPE: DNA
;   ORGANISM: AAP-5
US-09-819-308-9


  Query Match             81.1%;  Score 15.4;  DB 5;  Length 974;
  Best Local Similarity   94.1%;  Pred. No. 58;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCGCTCGGCCTGGTCCC 17
           |||||  ||||||||||
Db      21 gcgctaggcctggtccc 37


RESULT  14
US-09-543-679A-1740
; Sequence 1740, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
```

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;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;    INFORMATION FOR SEQ ID NO: 1740:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1740:
US-09-543-679A-1740


  Query Match             78.9%;  Score 15;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 TCGGCCTGGTCCCGG 19
          |||||||||||||||
Db      1 TCGGCCTGGTCCCGG 15


RESULT  15
US-09-739-449-6709
; Sequence 6709, Application US/09739449
; GENERAL INFORMATION:
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15490)C
;  CURRENT APPLICATION NUMBER: US/09/739,449
;  CURRENT FILING DATE:  2000-12-19
;  PRIOR APPLICATION NUMBER: US 09/514,000
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 6709
;   LENGTH: 303
;   TYPE: DNA
;   ORGANISM: Agrobacterium tumefaciens
US-09-739-449-6709


  Query Match             77.9%;  Score 14.8;  DB 5;  Length 303;
  Best Local Similarity   88.9%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GCGCTCGGCCTGGTCCCG 18
          ||||||||| |||| |||
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Db    121 gcgctcggcgtggtgccg 138


Search completed: April 20, 2001, 00:16:04
Job time: 9501 sec
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